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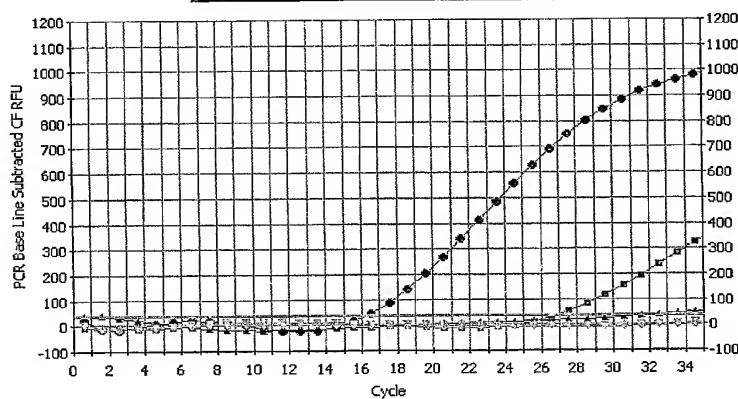
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[Continued on next page]

(54) Title: RAPID DETECTION OF MICROORGANISMS

PCR Amp/Cycle Graph for FAM-490



● *Zygosaccharomyces bailii*
(Lindner) Guilliermond [ATCC]
□ Industry-yeast
◇ B.F. (Mold)
▽ H₂O (Extraction)
▲ H₂O (non-extraction)

(57) Abstract: Tools and methods for detecting the presence bacteria, yeast and mold in a sample obtained from a food sample are provided. The methods employ a polymerase chain reaction and primer and probe sets that are based on the 16S rRNA and squalene-hopene cyclase genes of *Alicyclobacillus* and *Geobacillus* and the 18S rDNA gene of mold and yeast. The present invention also relates to primer and probe sets. Each primer and probe set comprises a forward primer and a reverse primer, both of which are from 15 to 35 nucleotides in length and a probe.



WO 2004/063699 A2



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RAPID DETECTION OF MICROORGANISMS**CROSS REFERENCE TO RELATED APPLICATIONS**

This application claims priority to U.S. Provisional Applications No. 60/xxxx, filed October 22, 2003, No. 60/500,736, filed September 05, 2003, and No. 60/430,202, filed December 02, 2002, each of which is incorporated herein by reference in their entirety.

TECHNICAL FIELD OF THE INVENTION

The present invention provides methods and tools for rapidly detecting microorganisms such as molds and fungi, and acid and thermophilic *Alicyclobacillus* spp and *Geobacillus* spp. in test samples, particularly food samples.

BACKGROUND

Spoilage of products, particularly food and beverage products, due to contamination with bacteria, yeasts and molds, results in significant financial loss to the food industry. Yeasts and molds are commonly associated with raw materials of foods and are often found in the processing environment. Due to the structural features of both the vegetative cells and spores of fungi, these food contaminants have a good chance of surviving current processing conditions. Yeasts and molds can grow within a wide range of environmental conditions, and therefore the presence in food of even minor amounts of yeast and mold contaminants can cause spoilage during storage.

Like fungi, many bacteria are resistant to processing conditions, and some are resistant even to high acid conditions in food and beverage products. *Alicyclobacilli* are Gram-positive, spore-forming, aerobic rods classified as thermoacidophiles capable of growing at high temperatures and low pH (1, 2, 3). These bacteria, formerly of the *Bacillus* genus, were assigned into the new genus *Alicyclobacillus* in 1992 (1). Sequence analysis of the 16s rRNA genes proved that three previously classified *Bacillus* thermoacidophiles (*B. acidocaldarius*, *B. acidoterrestris*, and *B. cycloheptanicus*) belong in a group that differs from other closely related *Bacilli*. Additionally, a key phenotypic variation was found in the membrane composition of these three species. The primary fatty acid component in the membrane was determined to be ω -alicyclic fatty acids, a type of lipid not found in other *Bacillus* species at the time. This evidence initiated the establishment of the *Alicyclobacillus* genus of obligate acidothermophiles, containing *A. acidocaldarius*, *A. acidoterrestris*, and *A. cycloheptanicus*, within the *Bacillus* branch (1). More recently, *A. hesperidum* and *Alicyclobacillus* genomic species 1 and 2 (24, 25), *A. acidiphilus* (22), *A. herbarius* (23), *A. sendaiensis* (26), and *A. pomorum* (27) have been added as new species within the genus *Alicyclobacillus*.

Alicyclobacilli have been an increasingly frequent spoilage problem in the beverage industry, particularly acidic juices, during the last two decades. In 1982, a *Bacillus* sporeformer

(to be later classified as *B. acidoterrestris* and then subsequently *A. acidoterrestris*) capable of growing at pH as low as 2.5 was isolated from apple juice (4, 5, 6). In 1994, Splittstoesser et al. discovered the presence of *A. acidoterrestris* in apple juice, further shown by Yamazaki et al. in 1996 (7, 8). Spore germination and growth in orange juice (3) and grapefruit juice (6) was even
5 observed. White grape juice, tomato juice, cranapple juice, and pear juice have also been afflicted with *Alicyclobacillus* spoilage (11).

While *Alicyclobacilli* are non-pathogenic, they are a spoilage agent that can drastically affect the quality of acidic fruit juices. Pettipher et al. (1997) reported that guaiacol, one of the chemicals responsible for the off-odor and smoky taints characteristic in *Alicyclobacillus*-spoiled
10 juices, can be detected by taste before any visible contamination is seen (3). Therefore, a consumer would generally not be able to identify *Alicyclobacillus*-spoiled juice until it is ingested. In addition to guaiacol, 2,6-dibromophenol (2,6-DBP) and 2,6-dichlorophenol (2,6-DCP) were found to contribute to disinfectant taints at detectable levels after as little as one day at 44°C in containers with large headspaces. More realistically, commercially stored shelf stable
15 juices with generally low headspace volume develop these taints within the first month of storage, particularly in warmer climates (10). The presence of these chemicals in *Alicyclobacillus*-spoiled juices significantly reduces the quality of the product, subsequently lowering the consumer image of the brand.

Alicyclobacilli are very heat resistant, growing from pH 2.5-5.5 and 25°C – 60°C (6).
20 Beyond growth, cells and spores can survive normal pasteurization procedures, at temperatures up to 97°C (3,6). Fruit juices that are fresh squeezed, pasteurized, or hot-filled are most easily affected by *Alicyclobacillus* spoilage, since ultra high temperature treatment is normally sufficient for killing all microorganisms (3). Since *Alicyclobacilli* can survive temperatures that exceed industry standard pasteurization specifications, contamination occurring before or during
25 the processing steps can lead to spoilage in the final product that reaches the consumer. Since significant increases in pasteurization temperatures or times ultimately affect product quality and flavor, companies aren't likely to change current procedures.

Early detection, i.e., before products reach the consumer, of the presence of even small amounts of these microbial contaminants in food and beverages is highly desirable in the food
30 industry. Classic culture methods are generally accurate for detecting the presence of microorganisms, but can take up to a week for the results. Previdi et al. (1997) reported a method for detecting *A. acidocaldarius* in juice products. This method required juices or concentrates to be heat treated and then incubated at 37°C for 7 days, followed by plating on pH 4.0 malt extract agar (13). Pinhatti et al. (1997) tested frozen orange juice concentrate by heat

shocking the samples at 80°C, enriching at 50°C for 24 and 48 h, and finally pour plating in BAM and incubating at 50°C for 24 h (12). Both of these methods of detection provided accurate results, but took from 3-7 days to complete. As with bacteria, it can often take one to two weeks just to grow yeast and mold cells on culture media. In addition, there are so many varieties of molds and yeasts with diverse growth requirements that it is very difficult to find an optimal medium to capture all potential yeast and mold contaminants at the same time. For food industry applications, it is desirable to have a rapid detection system that does not require time consuming culture techniques to detect the presence of microbial contamination of food samples. Accordingly, it is desirable to have a more rapid detection method that can provide results within a few hours, with the same level reliability of culture methods. It is also desirable to have kits that can differentiate between specific types of microbes and which comprise microbe-specific reagents that are useful for conducting rapid sample testing.

SUMMARY OF THE INVENTION

The present invention provides methods and kits for detecting the presence of *Alicyclobacillus* spp. and a closely related thermophilic bacterium, *Geobacillus*, in samples, particularly food samples. In one embodiment the method comprises, collecting bacterial cells in the sample, extracting DNA from the cells, and assaying for the presence of these bacterium species using a PCR technique, preferably real-time PCR, and three signature oligonucleotides (2 primers and a probe) directed to a particular sequence in a target gene encoding either the 16S rRNA or squalene-hopene cyclase (*shc*). (See the conserved sequences extending from nucleotide position 334 through nucleotide position 485, and from nucleotide position 752 through nucleotide position 813 of the *shc* gene sequence of *Alicyclobacillus* shown in Figure 5. Also see the conserved sequences extending from nucleotide position 1327 through nucleotide position 1460 of the 16S rRNA gene sequence of *Alicyclobacillus* shown in Figure 1.) The presence of multiple *Alicyclobacillus* spp. and a closely related thermophilic bacterium *Geobacillus* can be achieved within 3-5 hours using the described sample preparation procedures, and proper combination of the three oligonucleotides as primer-and-probe set in the real-time PCR reaction.

The kits of the present invention comprise at least one forward primer and one reverse primer, with or without a probe for amplifying a sequence of at least 50 consecutive nucleotides within a conserved region of the three *Alicyclobacillus* spp. shown in Figure 1 (sequences shown in alignment). Figures 2, 3 and 4, respectively, show the full coding sequences for the 16S rRNA genes from the *Alicyclobacillus* strains deposited with the ATCC as 43030, 49025, and 49029. In certain embodiments, the oligonucleotides comprise the entire or a majority of the following

sequences or their reverse complement sequences, as a set or as combination crossing multiple sets, e.g. in certain cases the forward primer of one set can be combined with a reverse primer that is based on the forward primer of another set. Thus the following embodiments can be used in various primer, probe, or primer-probe combinations. Depending on the primers that are combined, the lower oligo may be used as a probe. The sequence of the lower oligo corresponds to the coding sequence of the target region of the gene, and is complementary to the reverse primer in each set. The reverse primers are shown as the reverse complement of the targeted region of the gene. The forward primers correspond to the coding sequence of the target region of the gene.

Table I: Signature Oligonucleotides Directed Toward 16S rRNA gene

		Length	Tm(°C)	GC%
	Set 1:			
	Forward primer: 5'GAGCCCGCGGCGCATTAGC3'	19	68.9	73.7 (SEQ ID NO 1)
	Probe: 5'GCGACGATGCGTAGCC(G)3'	16	61.8	68.8 (SEQ ID NO 2)
15	Lower Oligo: 5'CGCAATGGGCGCAAGC3'	16	61.8	68.8 (SEQ ID NO 3)
	Reverse primer: 5'GCTTGCGCCCATTGCG3'	16	61.8	61.8 (SEQ ID NO 4)
	Set 2:			
	Forward primer: 5'GAGCAACGCCGCGTGAGCG3'	19	68.8	73.7 (SEQ ID NO 5)
20	Probe: 5'CTTCGGGTTGTAAAGC3'	16	54.2	50 (SEQ ID NO 6)
	Lower Oligo: 5'CGGCTAACTACGTGC3'	15	56.2	60 (SEQ ID NO 7)
	Reverse primer: 5'GCACGTAGTTAGCCG5'	15	56.2	60 (SEQ ID NO 8)
	Set 3:			
25	Forward Primer: 5'AGTGCTGGAGAGGCAAGG3'	18	62.2	61.1 (SEQ ID NO 9)
	Probe: 5'CTGGACAGTGACTGACG3'	17	59.6	58.8 (SEQ ID NO 10)
	Lower Oligo 5'GCACGAAAGCGTGGGGAGCA	20	66.6	65 (SEQ ID NO 11)
	Reverse Primer: 5'TGCTCCCCACGCTTTCGTGC5'	20	66.6	65 (SEQ ID NO 12)
30	Set 4:			
	Forward Primer: 5'GGAGTACGGTCGCAAGACTG3'	20	64.5	60 (SEQ ID NO 13)
	Probe: 5'CGCACAAGCAGTGGAGC3'	17	62.0	64.7 (SEQ ID NO 14)
	Lower Oligo: 5'CAGGGCTTGACATC3'	14	52.6	57.1 (SEQ ID NO 15)
	Reverse Primer: 5'GATGTCAAGCCCTG3'	14	52.6	57.1 (SEQ ID NO 16)
35	Set 5:			
	Forward primer: 5'GGCGTAAGTCGGAGGAAGG3'	19	64.5	63.2 (SEQ ID NO 17)
	Probe: 5'ATGTCCTGGGCTACACACG3'	19	62.3	57.9 (SEQ ID NO 18)
	Reverse primer: 5'GCCTGCAATCCGAACCTACC5'	19	62.3	57.9 (SEQ ID NO 19)
40	Set CC16S:			
	Forward primer: 5'CGTAGTTTCGGATTGCAGGC3'	19	65.6	57.9 (SEQ ID NO 20)
	Probe: 5'CGGAATTGCTAGTAATCGCG3'	20	57.9	47.4 (SEQ ID NO 21)
	Lower Oligo: 5'CACGAGAGTCGGCAACAC3'	18	63.3	61.1 (SEQ ID NO 22)
45	Reverse primer: 5'GTGTTGCCGACTCTCGTG3'	18	62.2	61.1 (SEQ ID NO 23)

Set 6:

primer: 5'GATGATTGGGGTGAAG3'

16

54.2

50 (SEQ ID NO 24)

Table II: Signature Oligonucleotides Directed Toward squalene-hopene cyclase (shc) gene

5 These three oligonucleotides were further used as PCR primer pair and DNA probe in real-time PCR detection of *Alicyclobacillus* spp.

Forward Primer: 5' ATGCAGAGYTCGAACG 3' (SEQ ID NO 25)

Probe: 5' 6-FAM d [TCG(A)GAA(G)GACGTCACCGC] BHQ-1 3' (SEQ ID NO 26)

Reverse Primer: 5' AAGCTGCCGAARCACTC 3' (Y=C+T; R=A+G (SEQ ID NO 27)

10

Table III: The Sequence, GC% and Tm of Primer and probe set candidate 1 for Shc Gene:

Name	Sequence	Length	Tm	GC%
Forward primer	TACTGGTGGGGGCCGCT (SEQ ID NO 28)	17	64.84	70.59
	TACTGGTGGGCGCCGCT (SEQ ID NO 29)	17	64.84	70.59
Probe	ATGGAAGCGGAGTACGTCC (SEQ ID NO 30)	19	62.64	57.9
	ATGGAAGCGGAGTACGTCCT (SEQ ID NO 31)	20	62.45	55
	ATGGAAGCGGAATATGTGC (SEQ ID NO 32)	19	58.32	47.37
	ATGGAAGCGGAATATGTGCT (SEQ ID NO 33)	20	58.35	45
Reverse Primer	CGCGAGGACGGCAC (SEQ ID NO 34)	14	62.11	78.57
	CGCGAGGACGGCACGTGG (SEQ ID NO 35)	18	69.79	77.78
	CGCGAAGACGGCAC (SEQ ID NO 36)	14	59.16	71.43
	CGCGAAGACGGCACCTGG (SEQ ID NO 37)	18	67.51	72.22

15 **Table IV: The Sequence, GC% and Tm of Primer and probe set candidate 2 for Shc Gene:**

Name	Sequence	Length	Tm	GC%
Forward primer	CAAAAGGCGCTCGACTG (SEQ ID NO 38)	17	60.02	58.82
	CAAAAGGCGCTCGACTGG (SEQ ID NO 39)	18	62.96	61.11
	CAAAAGGCGCTCGACTGGGTCG (SEQ ID NO 40)	22	68.99	63.64
	CAAAAGTCGCTCGACTG (SEQ ID NO 41)	17	57.61	52.94
	CAAAAGTCGCTCGACTGG (SEQ ID NO 42)	18	60.68	55.56
	CAAAAGTCGCTCGACTGGCTCG (SEQ ID NO 43)	22	67.13	59.09
Probe	GGACGGCGGCTGGGGCGA (SEQ ID NO 44)	18	72.07	83.33
	GGACGGCGGCTGGGGCGAGGA (SEQ ID NO 45)	21	75.09	80.95
	GGACGGCGGCTGGGGCGAGGACTGCCG (SEQ ID NO 46)	27	80.31	81.48
	GGATGGCGGTTGGGGTGA (SEQ ID NO 47)	18	65.23	66.67
	GGATGGCGGTTGGGGTGAAGA (SEQ ID NO 48)	21	67.28	61.91

	GGATGGCGGTTGGGGTGAAGATTGCCG (SEQ ID NO 49)	27	72.72	62.96
Reverse Primer ^a	TGATGGCGCTCATCGC (SEQ ID NO 50)	16	59.53	62.5
1	TGATGGCGCTCATCGCGGGCGGC (SEQ ID NO 51)	23	74.2	73.91
2	ACCCGTCGCAGACGGCCTGGGCGC (SEQ ID NO 52)	25	77.7	80
3	ACACCGTCGCAGACCGCCTGGGCGT (SEQ ID NO 53)	25	74.42	72

The present invention also provides methods and kits for detecting the presence of yeast and mold contaminants in samples, particularly in food samples. In one aspect, the method comprises collecting particulate matter, preferably cells and cellular fragments, in the sample, extracting DNA from the particulate matter, and assaying for the presence of yeast DNA in the extracted DNA using a PCR technique using primers that amplify a select conserved region in 18s rDNA of representative yeast species, including *Zygosaccharomyces bailii* (Lindner) Guilliermond strain ATCC 36947 and the other yeast species shown Figure 7. (See conserved sequence extending from nucleotide 81 through nucleotide 225 of the sequence of *Z. bali*.) Preferably, the method uses real-time PCR, and three signature oligonucleotides (2 primers and a probe) directed to a particular sequence in the gene encoding the yeast 18S rDNA.

In another aspect, the kit of the present invention comprise at least one forward primer and one reverse primer, with or without a probe for amplifying a sequence of at least 50 consecutive nucleotides within the select region of yeast 18s rDNA. In one embodiment, the kit comprises primers and a probe having the following sequences:

Yupreal: 5' GTGGTGCTAGCATTTGCTG 3' (SEQ ID NO 54)

Ylowreal: 5' GTTAGACTCGCTGGCTCC 3' (SEQ ID NO 55)

Yprobe: 5' TTCAAGCCGATGGAAGTTTGA(C/G)3' (SEQ ID NO 56)

Another probe that may be used in the present method has the following sequence

5' CGGTTTCAAGCCGATGGAAGT 3'. (SEQ ID NO 57)

Yet another set of primers and probe for yeast detection:

Oligo name

Len Pur Scale Sequence (5'-3')

18srRNA-newup-112503-1

30 DST 0.05 CCTACTAAATAGGGTGCTAGCATTTGCTGG (SEQ ID NO 58)

18srRNA- newup-112503-2

26 DST 0.05 CTAAATAGGGTGCTAGCATTTGCTGG (SEQ ID NO 59)

18srRNA-probe2

25

CGGTTTCAAGCCGATGGAAGTTTGA (SEQ ID NO 60)

In another aspect the present method comprises collecting particulate matter, preferably cells and cellular fragments, in the sample, extracting DNA from the particulate matter, and assaying for the presence of mold DNA in the extracted DNA using a PCR technique using primers that amplify a select conserved region in 18s rDNA of the following representative molds: *Byssoschlamys fulva* Olliver et Smith, teleomorph ATCC 24474 and *Penicillium digitatum* Saccardo, anamorph ATCC10030, as shown in the attached alignment. (See the conserved sequence extending from nucleotide 114 through nucleotide 239 of the 18s rDNA sequence of *P. digitatum* shown in Figure 7.) Preferably, the method uses real-time PCR, and three signature oligonucleotides (2 primers and a probe) directed to a particular sequence in the gene encoding the mold 18s rDNA.

In another aspect, the present the kits of the present invention comprise at least one forward primer and one reverse primer, with or without a probe for amplifying a sequence of at least 50 consecutive nucleotides within the select region of mold 18s rDNA. In one embodiment, the kit comprises primers and a probe having the following sequences:

Mupreal: 5' CCGCTGGCTTCTTAGGG 3' (SEQ ID NO 61)

Mlowreal: 5' AGGGCCAGCGAGTACATCA 3' (SEQ ID NO 62)

Mprobe: 5' CTCAAGCCGATGGAAGTGCG 3' (SEQ ID NO 63)

The invention further provides a method for detecting through real-time PCR using at least one of the nucleic acid primer pairs, and at least one probe, the presence of acidophilic bacterium in a test sample, especially in a food sample. In one embodiment, the acidophilic bacterium detection method includes use of one forward primer directed to the 16S rRNA gene, wherein the primer is selected from the forward primers listed in Table I, one reverse primer directed to the 16S rRNA gene wherein the primer is selected from the reverse primers listed in Table I, and one probe directed to a sequence that is located between the sequences to which the forward and reverse primers are directed, wherein the probe is selected from the group of probes listed in Table I.

In another embodiment, the acidophilic bacterium detection method includes use of one forward primer directed to the squalene-hopene cyclase gene, wherein the forward primer is selected from the group of forward primers listed in Tables II and III, one reverse primer directed to the squalene-hopene cyclase gene wherein the primer is selected from the group of reverse primers listed in Tables II and III, and one probe directed to a sequence that is located between

the sequences to which the forward and reverse primers are directed, wherein the probe is selected from the group of probes listed in Tables II and III.

In yet another embodiment, the acidophilic bacterium detection method includes use of one forward primer directed to the squalene-hopene cyclase gene, wherein the forward primer is selected from the group of forward primers listed in Table IV, one reverse primer directed to the squalene-hopene cyclase gene wherein the primer is selected from the group of reverse primers listed in Table IV, and one probe directed to a sequence that is located between the sequences to which the forward and reverse primers are directed, wherein the probe is selected from the group of probes listed in Table IV.

In another embodiment, the yeast detection method includes use of one forward primer directed to the 18S rDNA gene, wherein the primer is selected from the group consisting of SEQ ID NO 54 and SEQ ID NO 58, one reverse primer directed to the 18S rDNA gene wherein the primer is selected from the group of consisting of SEQ ID NO 55 and SEQ ID NO 55, and one probe directed to a sequence that is located between the sequences to which the forward and reverse primers are directed, wherein the probe is selected from the group consisting of SEQ ID NO 56, SEQ ID NO 57 and SEQ ID NO 60.

In yet another embodiment, the mold detection method includes use of one forward primer directed to the 18S rDNA gene, wherein the primer corresponds to SEQ ID NO 61, one reverse primer directed to the 18S rDNA gene wherein the primer corresponds to SEQ ID NO 62, and one probe directed to a sequence that is located between the sequences to which the forward and reverse primers are directed, wherein the probe corresponds to SEQ ID NO 63.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows polynucleotide sequence alignment of 16S rRNA gene fragments from three representative strains of *Alicyclobacillus*, specifically, *A. acidocaldarius* ATCC43030, *A. acidoterrestris* ATCC49025, and *A. cycloheptanicus* ATCC49029

Figure 2 shows the 16S rRNA gene coding Sequence for *A. cycloheptanicus* ATCC49029

Figure 3 shows the 16S rRNA gene coding Sequence for *A. acidoterrestris* ATCC49025

Figure 4 shows the 16S rRNA gene coding Sequence for *A. acidocaldarius* ATCC43030

Figure 5: shows the Shc gene sequence alignments for *A. cycloheptanicus* ATCC49029 and *A. acidoterrestris* ATCC49025

Figure 6: shows the Shc amino acid sequence alignments for *A. cycloheptanicus* ATCC49029 and *A. acidoterrestris* ATCC49025

Figure 7 shows the alignment for the 18s rDNA gene coding Sequence for *Zygosaccaromyces*, *Penicillium digitatum*, and *Byssochlamys fulva*

Figure 8 shows the 16S rRNA gene coding sequence alignments for several strains of for *A. cycloheptanicus*

Figure 9. shows the results of Real-time PCR detection of *A. acidocaldarius* (black), *A. cycloheptanicus* (blue), and *A. acidoterrestris* (lt. green) using the CC16S specific probe

5 and primer pair.

Figure 10 shows the results of Real-time PCR sensitivity test of *A. acidoterrestris* using the CC16S primers and probe

Figure 11 shows the results of Real-time PCR sensitivity test of *A. acidoterrestris* in orange juice.

10 Figure 12 shows the 18s rDNA gene coding Sequence for *Zygosaccaromyces*

Figure 13 shows the 18s rDNA gene coding Sequence for *Penicillium digitatum*

Figure 14 shows the 18s rDNA gene coding Sequence for *Byssoschlamys fulva*

Figure 15 shows the results of a specificity test. ◊ *Zygosaccharomyces bailii* (Lindner) Guilliermond ATCC 36947; □ industry sample yeast. ◇ *Byssoschlamys fulva* Olliver et Smith
15 ATCC 24474; ▽ H₂O control with extraction. ▲ H₂O control without extration.

Figure 16 shows the results of a specificity test with ▼ yeast, ◆ mold and acciobacillus and ▲ H₂O

Figure 17 shows the results of a specificity test with □ Z.b(yeast).; ▲ B.F.(mold); ◇ Accidobacillus; ▽ water; Apple; ▽ green grape; and ■ Red grape.

20 Figure 18 shows the results of a specificity test with □ Z.b.; ▲ B.F.; ◇ Accidobacillus and

Figure 19 shows the results of a specificity test with ■ Orange1; △ Orange2; ◇ Orange Juice Supernatant; ● Orange Juice pellet; ○ Yeast; and ▼ H₂O

Figure 20 shows the results of a specificity test with !*Byssoschlamys fulva* Olliver et Smith, telomorph ATCC 24474; *Penicillium digitatum* Saccardo, anamorph ATCC 10030; #*Zygosaccharomyces bailii* (Lindner) Guilliermond, telomorph deposited as *Saccharomyces bailii* Lindner, telomorph ATCC 36947; %Industry Mold 42; &Indusrty Mold 41; "Industry Mold 3; "Water (extracted); %water (not extracted)

Figure 21 shows specificity test results with *Bussochlamys fulva* Olliver et Smith, teleomorph
30 ATCC24474; water and *Zygosaccharomyces bailii* (Lindner) Guilliermond, telomorph deposited as *Saccharomyces bailii* Lindner, telomorph ATCC 36947; *Acidobacillus acidoterrestris* 49025.

Figure 22 shows the Alignment^a of 134 bp priming region flanked by CC16S-F (CGTAGTTCGGATTGCAGGC), CC16S-Probe (CGGAATTGCTAGTAATCGC), and CC16S-R (CACGAGAGTCGGCAACAC)^b.

Figure 23 shows the results of Real-time PCR detection of *A. acidocaldarius* ATCC 43030 (●), *A. cycloheptanicus* ATCC 49029 (◆), and *A. acidoterrestris* ATCC 49025 (■) using the CC16S primer and probe set.

Figure 24 shows the results of Real-time PCR sensitivity test of *A. acidoterrestris* ATCC 49025 in saline solution using the CC16S primers and probe

Figure 25 shows the results of Real-time PCR sensitivity test of *A. acidoterrestris* ATCC 49025 in orange juice, using the CC16S primers and probe.

Figure 26 shows the results of Real-time PCR detection of food-borne microorganisms using the developed primer-and-probe set.

Figure 27 shows the results of Real-time PCR sensitivity test

Fig. 28. Real-time PCR detection of *A. acidocaldarius* ATCC43030 cells in apple juice using *shr*-specific primer-and-probe set.

DETAILED DESCRIPTION OF THE INVENTION

The methods and kits provided herein enable the rapid and reliable detection of contaminating microorganisms that are found in test samples of products, preferably consumer products, and most preferably food products. The methods are especially suited for the detection of *Alicyclobacillus* spp. including *A. acidocaldarius*, *A. acidoterrestris*, *A. cycloheptanicus*, *A. hesperidum*, *A. acidiphilus*, *A. herbarius*, *A. sendaiensis*, and *A. pomorum* and *Geobacillus stearothermophilus*, and a variety of yeasts and mold. Other reported methods use conventional PCR (using a pair of oligonucleotides as primers) to detect the presence of *Alicyclobacillus* spp. (Obara and Niwa, 1998) which usually is associated with the problem of high background with non-specific PCR products.

According to the methods described herein, a sample is obtained from a test material, for example a sample of a fruit juice or other food product. The sample is processed to extract any polynucleotides in the sample, particularly polynucleotides from target organisms that may be present in the material. After extraction and processing according to methods described herein or otherwise known in the art, the sample is treated with reagents that comprise a forward primer, oligonucleotide, a reverse primer oligonucleotide, and a labeled oligonucleotide probe, wherein the reagents are targetted for specific regions within the genome of target organisms. The sample is then processed according to PCR amplification methods. The PCR product is first amplified using the primers. Binding of the labeled probe to a target sequence within the PCR product that corresponds with a target region in the genomic DNA of the contaminating bacteria or mold signals the presence of contaminating microorganisms.

Therefore the combination of the three unique sequences and the real-time PCR technology ensured specific and sensitive detection of the presence of the target bacteria. This real-time PCR approach also offers other features such as a) accuracy: more than one probe will be included in the detection system with less possible error; b) flexibility: up to four PCR products can be simultaneously detected so potentially incorporating probes for other spoilage microorganisms into the detection system is expected.

Primer Selection

Primers are selected within the conserved regions shown in the attached alignment (Figure 1) to amplify a fragment with proper size for optimal detection. One primer is located at each end of the sequence to be amplified. Such primers will normally be between 10 to 35 nucleotides in length and have a preferred length from between 18 to 22 nucleotides. The smallest sequence that can be amplified is approximately 50 nucleotides in length (e.g., a forward and reverse primer, both of 20 nucleotides in length, whose location in the sequences is separated by at least 10 nucleotides). Much longer sequences can be amplified. Preferably, the length of sequence amplified is between 75 and 250 nucleotides in length, and between 75 and 150 for Taqman assay.

One primer is called the “forward primer” and is located at the left end of the region to be amplified. The forward primer is identical in sequence to a region in the top strand of the DNA (when a double-stranded DNA is pictured using the convention where the top strand is shown with polarity in the 5’ to 3’ direction). The sequence of the forward primer is such that it hybridizes to the strand of the DNA which is complementary to the top strand of DNA.

The other primer is called the “reverse primer” and is located at the right end of the region to be amplified. The sequence of the reverse primer is such that it is complementary in sequence to, i.e., it is the reverse complement of a sequence in, a region in the top strand of the DNA. The reverse primer hybridizes to the top strand of the DNA.

PCR primers should also be chosen subject to a number of other conditions. PCR primers should be long enough (preferably 10 to 30 nucleotides in length) to minimize hybridization to greater than one region in the template. Primers with long runs of a single base should be avoided, if possible. Primers should preferably have a percent G+C content of between 40 and 60%. If possible, the percent G+C content of the 3’ end of the primer should be higher than the percent G+C content of the 5’ end of the primer. Primers should not contain sequences that can hybridize to another sequence within the primer (i.e., palindromes). Two primers used in the same PCR reaction should not be able to hybridize to one another. Although PCR primers are preferably chosen subject to the recommendations above, it is not necessary that the primers

conform to these conditions. Other primers may work, but have a lower chance of yielding good results.

PCR primers that can be used to amplify DNA within a given sequence can be chosen using one of a number of computer programs that are available. Such programs choose primers that are optimum for amplification of a given sequence (i.e., such programs choose primers subject to the conditions stated above, plus other conditions that may maximize the functionality of PCR primers). One computer program is the Genetics Computer Group (GCG recently became Accelrys) analysis package which has a routine for selection of PCR primers. There are also several web sites that can be used to select optimal PCR primers to amplify an input sequence. One such web site is <http://alces.med.umn.edu/rawprimer.html>. Another such web site is http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi.

Making the Oligonucleotide Primers and Probes

The oligonucleotide primers and probes disclosed in this application can be made in a number of ways. One way to make these oligonucleotides is to synthesize them using a commercially-available nucleic acid synthesizer. A variety of such synthesizers exists and is well known to those skilled in the art. Many such synthesizers use phosphoramidite chemistry, although other chemistries can be used. Phosphoramidite chemistry utilizes DNA phosphoramidite nucleosides, commonly called monomers, to synthesize the DNA chain or oligonucleotide. Such monomers are modified with a dimethoxytrityl (DMT) protecting group on the 5'-end, a *b*-cyanoethyl protected 3'-phosphite group, and may also include additional modifiers that serve to protect reactive primary amines in the heterocyclic ring structure (to prevent branching or other undesirable side reactions from occurring during synthesis).

To make an oligonucleotide of a specific sequence, phosphoramidite nucleosides are added one-by-one in the 3'-5' direction of the oligonucleotide, starting with a column containing the 3' nucleoside temporarily immobilized on a solid support. Synthesis initiates with cleavage of the 5'-trityl group of the immobilized 3' nucleoside by brief treatment with acid [dichloroacetic acid (DCA) or trichloroacetic acid (TCA) in dichloromethane (DCM)] to yield a reactive 5'-hydroxyl group. The next monomer, activated by tetrazole, is coupled to the available 5'-hydroxyl and the resulting phosphite linkage is oxidized to phosphate by treatment with iodine (in a THF/pyridine/H₂O solution). The above describes the addition of one base to the oligonucleotide. Additional cycles are performed for each base that is added. The final oligonucleotide added does not have a 5' phosphate. When synthesis is complete, the oligonucleotide is released from the support by ammonium hydroxide and deprotected (removal of blocking groups on nucleotides).

Normally, oligonucleotides of up to 150-180 bases long can be efficiently synthesized by this method using a nucleic acid synthesizer. To make oligonucleotide that are longer than 100 bases, two single-stranded oligonucleotides, that are partially complementary along their length, can be synthesized, annealed to one another to form a duplex, and then ligated into a plasmid vector. Once a plasmid containing the ligated duplexes has been formed, additional oligonucleotide duplexes can be ligated into the plasmid, adjacent to the previously ligated duplexes, to form longer sequences. It is also possible to sequentially ligate oligonucleotide duplexes to each other, to form a long, specific sequence, and then clone the single long sequence into a plasmid vector.

10 Sample preparation flow chart for bacteria detection

Collect cells by centrifugation or membrane filtration



Lyse Cells using standard techniques



15

DNA extraction using standard techniques



Analysis (Real-time PCR)

Sample preparation flow chart for fungi (yeast and mold) detection

Collect cells and cell fragments by centrifugation or membrane filtration



20

Lyse Cells using standard techniques



Extract DNA using standard techniques



25

Analysis (Real-time PCR)

Isolation of DNA from Samples

DNA is isolated or extracted from the microorganism cells contained within the test sample. For example, DNA extraction may be performed using any of numerous commercially available kits for such purpose. One such kit, called IsoCode, is available from Schleicher and Schuell of Keene, New Hampshire. The IsoCode kit contains paper filters onto which cells are applied. Through treatment of the paper filters as described by the manufacturer, most cellular components remain in the paper filter and DNA is released into an aqueous solution. The DNA in the solution can then be added to various enzymatic amplification reactions, as are discussed below.

Other commercially available kits exist for extraction of DNA from cells. Commercial kits do not have to be used, however, in order to obtain satisfactory DNA. Standard methods, well known to those skilled in the art, have been published in the scientific literature. Such methods commonly involve lysis of cells and removal of cellular components other than nucleic acids by precipitation or by extraction with organic solvents. Enzymatic treatment with proteases and ribonucleases can be used to remove proteins and RNA, respectively. DNA is then commonly precipitated from the sample using alcohol.

Real-Time PCR

A variety of methods can be used to determine if a PCR product has been produced. One way to determine if a PCR product has been produced in the reaction is to analyze a portion of the PCR reaction by agarose gel electrophoresis. For example, a horizontal agarose gel of from 0.6 to 2.0% agarose is made and a portion of the PCR reaction mixture is electrophoresed through the agarose gel. After electrophoresis, the gel is stained with ethidium bromide. PCR products are visible when the gel is viewed during illumination with ultraviolet light. By comparison to standardized size markers, it is determined if the PCR product is of the correct expected size.

The PCR procedure preferably is done in such a way that the amount of PCR products can be quantified. Such "quantitative PCR" procedures normally involve comparisons of the amount of PCR product produced in different PCR reactions. A number of such quantitative PCR procedures, and variations thereof, are well known to those skilled in the art. One inherent property of such procedures, however, is the ability to determine relative amounts of a sequence of interest within the template that is amplified in the PCR reaction.

One particularly preferred method of quantitative PCR used to quantify copy numbers of sequences within the PCR template is a modification of the standard PCR called "real-time PCR." Real-time PCR utilizes a thermal cycler (i.e., an instrument that provides the temperature changes necessary for the PCR reaction to occur) that incorporates a fluorimeter (i.e. an instrument that measures fluorescence). In one type of real-time PCR, the reaction mixture also contains a reagent whose incorporation into a PCR product can be quantified and whose quantification is indicative of copy number of that sequence in the template. One such reagent is a fluorescent dye, called SYBR Green I (Molecular Probes, Inc.; Eugene, Oregon) that preferentially binds double-stranded DNA and whose fluorescence is greatly enhanced by binding of double-stranded DNA. When a PCR reaction is performed in the presence of SYBR Green I, resulting DNA products bind SYBR Green I and fluoresce. The fluorescence is detected

and quantified by the fluorimeter. Such technique is particularly useful for quantification of the amount of template in a PCR reaction.

A preferred variation of real-time PCR is TaqMan® (Applied Biosystems) PCR. The basis for this method is to continuously measure PCR product accumulation using a dual-labeled
5 flourogenic oligonucleotide probe called a TaqMan® probe. The “probe” is added to and used in the PCR reaction in addition to the two primers. This probe is composed of a short (ca. 15-30 bases) oligodeoxynucleotide sequence that hybridizes to one of the strands that are made during the PCR reaction. That is, the oligonucleotide probe sequence is homologous to an internal target sequence present in the PCR amplicon. The probe is labeled or tagged with two different
10 flourescent dyes. On the 5' terminus is a “reporter dye” and on the 3' terminus is a “quenching dye.” One reporter dye that is used is called 6-carboxy fluorescein (FAM). One quenching dye that is used is called 6-carboxy tetramethyl-rhodamine (TAMRA). When the probe is intact, energy transfer occurs between the two fluorochromes and emission from the reporter is quenched by the quencher, resulting in low, background fluorescence. During the extension
15 phase of PCR, the probe is cleaved by the 5' nuclease activity of Taq polymerase, thereby releasing the reporter from the oligonucleotide-quencher and producing an increase in reporter emission intensity. During the entire amplification process the light emission increases exponentially.

Because the detection in Taqman assay is based on complementary binding of the third
20 oligonucleotide probe to the amplified PCR products, it can significantly minimize false positive results due to the detection of non-specific amplification and primer dimers in conventional PCR and other non-specific real-time PCR product detection approaches such as using SYBR Green or EtBr. However, the determination of proper primer and probe set needs more specified skills so that they will fit the product amplification and signal detection requirements.

25 Examples of primers and probes that are particularly useful in this procedure are listed above.

Fluorescence Detection

One example of an instrument that can be used to detect the fluorescence is an ABI Prism 7700, which uses fiber optic systems that connect to each well in a 96-well PCR tray format. The
30 laser light source excites each well and a CCD camera measures the fluorescence spectrum and intensity from each well to generate real-time data during PCR amplification. The ABI 7700 Prism software examines the fluorescence intensity of reporter and quencher dyes and calculates the increase in normalized reporter emission intensity over the course of the amplification. The results are then plotted versus time, represented by cycle number, to produce a continuous

measure of PCR amplification. To provide precise quantification of initial target in each PCR reaction, the amplification plot is examined at a point during the early log phase of product accumulation. This is accomplished by assigning a fluorescence threshold above background and determining the time point at which each sample's amplification plot reaches the threshold (defined as the threshold cycle number or CT). Differences in threshold cycle number are used to quantify the relative amount of PCR target contained within each tube.

Detecting fungi in samples

Oligonucleotide primer and probe development for detecting yeast

We have cloned and sequenced the 18S rDNA gene fragments from representative yeast *Zygosaccharomyces bailii* (Lindner) Guilliermond strain ATCC 36947. We then compared our sequences against other published 18S rDNA sequences from molds, yeasts, and common eukaryotic foods. We have also compared other target sequences including h1, h2, 23S rDNA, spacer sequence between 18S and 23S rDNA gene. We have developed primer-and-probe sequences that can detect the presence of generally all yeasts without cross-reacting with foods, molds or other bacteria. The aligned sequences of the 18S rDNA sequences of these yeast species are shown in Figure 17. Figures 12, 13 and 14 show the full coding sequences for the genes corresponding to the alignments shown in Figure 17.

Specificity Testing

Using the primer pair-and-probe set, all yeasts were tested positive in real-time PCR (Figures 15-19), while no cross-reaction was detected in other commonly found foodborne microorganisms and food items (Figures 15-19). Further specificity study revealed no combination of the above three oligonucleotides in other microorganisms after blast searching the nucleotide sequence database in the GenBank.

Oligonucleotide primer and probe development for detecting mold

We have cloned and sequenced the 18S rDNA gene fragments of representative molds of food industry concerns, *Byssochlamys fulva* Olliver et Smith, teleomorph ATCC 24474 and *Penicillium digitatum* Saccardo, anamorph ATCC10030. Cloning primer up:TGCATGGCCGTTCTTAGTTGG(Z.B. code 64-75) (B.F. 667-688) (P.D. 674-695) down: GTGTGTACAAAGGGCAGGG(Z.B. 417-237) (B.F. 1011-1031) (P.D. 1029-1049). We then compared our sequences against other published 18S rDNA sequences from molds, yeasts, and common eukaryotic foods. We have also compared other target sequences including h1, h2, 23S rDNA, spacer sequence between 18S and 23S rDNA gene. We have developed primer and probe sequences that can detect the presence of generally all mold without cross-reacting with foods, yeast or bacteria.

Specificity test

Using primer pair-and-probe set, all yeasts were tested positive in real-time PCR (Figures 20 and 21), while no cross-reaction was detected in other commonly found foodborne microorganisms and food items (Figures 20 and 21). Further specificity study revealed no combination of the above three oligonucleotides in other microorganisms after blast searching the nucleotide sequence database in the GenBank.

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EXAMPLES

Example 1:

10 In this study, the 16s rDNA sequences of *A. acidocaldarius*, *A. cycloheptanicus*, and *A. acidoterrestris* were used as models for the development of specific primers and a flourogenic probe to be used in a real-time PCR assay. 16s rDNA was isolated from ATTC strains 43030, 49025, and 49029, then cloned into vectors, transformed into competent cells, and purified for sequencing. Following sequencing, the 16s rDNA sequences of the three strains were analyzed for the development of oligonucleotide primers and a flourescent probe. These primers and
15 probe were used in a real-time PCR detection system where specificity and sensitivity tests were performed in media as well as beverage systems. This rapid detection system is unique because it can specifically detect not only the three original *Alicyclobacillus* species, but also detects newer species of *Alicyclobacillus* because of the genus-level 16s rDNA conservation of the priming sequences. This system can greatly benefit the food industry, particularly the beverage
20 industry, by detecting the presence of *Alicyclobacillus* within hours, before the product ever reaches the consumer, saving not only time and money, but maintaining brand image and quality.

Materials and Methods

Bacterial strains and culture conditions. *A. acidocaldarius* strain ATTC 43030 was grown on ATCC 573 medium, consisting of 1.3g (NH₄)₂SO₄, 0.37g KH₂PO₄, 0.25g MgSO₄·7H₂O, 0.07g
25 CaCl₂·2H₂O, 1.0g glucose, 1.0g yeast extract, and 1.0 L distilled H₂O. Solution pH was adjusted to 4.0 using H₂SO₄ and autoclaved at 121°C for 15 minutes. *A. acidoterrestris* strain ATTC 49025 and *A. cycloheptanicus* strain ATCC 49029 were grown on BAM-SM ATCC 1656 medium consisting of 0.25g CaCl₂·2H₂O, 0.5g MgSO₄·7H₂O, 0.2g (NH₄)₂SO₄, 3.0g KH₂PO₄, 6.0g yeast extract, 5.0g glucose, 1.0mL trace elements (0.66g CaCl₂·2H₂O, 0.18g ZnSO₄·7H₂O, 0.16g
30 CuSO₄·5H₂O, 0.15g MnSO₄·4H₂O, 0.18g CoCl₂·6H₂O, 0.10g H₃BO₃, 0.30g Na₂MoO₄·2H₂O, 1.0L distilled H₂O), and 1.0L distilled H₂O. Solution pH was adjusted to 4.0 using H₂SO₄ and autoclaved at 121°C for 15 minutes. Stock cultures of all strains were stored in their respective media plus 40% glycerol and kept at -80°C.

Isolation of genomic DNA and amplification of 16s rDNA. DNA was isolated from 2% cultures
35 of *A. acidoterrestris* strain ATTC 49025, *A. cycloheptanicus* strain ATCC 49029 *A. acidocaldarius* strain ATTC 43030 in respective media. Cultures were grown for 24 hours at

47°C. Genomic DNA was extracted from each strain using the Qiagen DNeasy Tissue Kit (Qiagen, Valencia, CA). The included protocol was followed, except the elution was repeated once with 100µl of buffer AE. An approximately 1,500 bp region of the 16s rDNA was amplified from the genomic DNA using primers 8F and 1492R (15) with PCR performed on the Bio-Rad iCycler Thermal Cycler (Bio-Rad Laboratories, Hercules, California). A 50µl reaction mixture was used, containing 0.5µl of primer 8F, 0.5µl of primer 1492R, 1.0µl of genomic DNA, 37µl of sterile H₂O, 3µl of 50mM MgCl₂, 2µl of a 10mM dNTP mixture, and 1.0µl Taq polymerase (Invitrogen, Carlsbad, CA). Amplification conditions included 30 cycles of 95°C for 2 min, 42°C for 30 s, and 72°C for 4 min, with a final chain elongation for 20 min (15). PCR products were confirmed after 20 min of gel electrophoresis on 0.9% agarose gel at 100 volts, followed by 10 min of ethidium bromide staining for visualization.

Cloning and transformation of 16s rDNA gene. PCR products were purified using the QIAquick PCR purification kit (Qiagen, Valencia, CA). The protocol was followed as specified by the manufacturer, except 30µl of sterile H₂O was used in place of 50µl of buffer EB for a single elution. Purified PCR products were then cloned into pCR 2.1 vectors using the TA Cloning kit (Invitrogen, Carlsbad, CA). A 10 µl ligation reaction for each PCR product was prepared as follows: 5µl sterile H₂O, 1µl pCR 2.1 vector, and 2µl PCR product were mixed together and incubated at 65°C for 5 min, followed by 10 min of incubation on ice. 1µl 10X ligation buffer and 1µl T4 DNA ligase were then added to the mixture, followed by overnight incubation at 14°C. Transformation was then performed, beginning with centrifugation of the ligation reactions. Reactions were stored on ice while 50µl of One Shot competent *Escherichia coli* cells were thawed for each transfer. 5µl of each ligation reaction was added to a vial of One Shot cells and mixed gently, followed by incubation for 30 min on ice. Reactions were then heat shocked for 30 s at 42°C, and then placed on ice. 200µl of SOC medium was added to each tube and then shook at 200 rpm for one hour at 37°C. The whole vial of cells was then spread onto LB agar plates containing X-Gal (20mg/ml) and incubated at 37°C overnight. Plates were stored at 4°C following incubation.

Sequencing of 16s rDNA gene. Plates were observed for transformed (white) colonies. Five transformed colonies from each plate were selected using a sterile toothpick, then dipped into a microfuge tube containing 100µl of sterile H₂O, and also spread on an LB agar plate. The stick was then placed into a tube containing 2ml of LB broth and ampicillin (50mg/ml). Plates were incubated at 37°C overnight. LB tubes were shaken at 100 rpm at 37°C overnight. Microfuge tubes were incubated at 100°C for 10 min, followed by PCR to check for successful

transformation. Standard 3-step PCR (CYCLES) was run with a 50µl reaction mixture containing 0.5µl of primer M13F, 0.5µl of primer M13R, 1.0µl of transformed DNA, 37µl of sterile H₂O, 3µl of 50mM MgCl₂, 2µl of a 10mM dNTP mixture, and 1.0µl Taq polymerase (Invitrogen, Carlsbad, CA). PCR products were analyzed by gel electrophoresis. LB tubes were centrifuged for 10 min at 6000 rpm after overnight incubation and used in the QIAprep Spin Miniprep kit (Qiagen, Valencia, CA) following the manufacturer's protocol. 5µl of product was set aside for PCR, and the rest of the miniprep yield was sent to be sequenced. Sequence data was entered into the NCBI BLAST network to search for similar sequences. Cloned sequences from ATCC strains 49025, 49029, and 43030 matched multiple 16s rDNA sequences from *Alicyclobacillus* species on the BLAST network.

Real-time Taqman PCR conditions. Fifty microliter reaction mixtures containing 0.5µl of a 100µM solution of CC16S-F primer, 0.5µl of a 100µM solution of CC16S-R primer, 0.5µl of a 100µM solution of CC16S-Probe, 33.3µl of sterile H₂O, 5.0µl of genomic DNA, 5µl of 10X reaction buffer, 3µl of MgCl₂, 2µl of dNTP's, and 0.2µl of Taq polymerase (Invitrogen, Carlsbad, CA) were used for specificity tests. For sensitivity assays, the following 50µl reaction mixtures were used: 25µl of 2X iQ Supermix, containing 100 mM KCl, 40 mM Tris-HCl, pH 8.4, 0.4 mM each dNTP, 50 U/ml iTaq DNA polymerase, 6 mM MgCl₂, and stabilizers (Bio-Rad, Hercules, CA), 0.5µl of 100µM stock CC16S-F primer, 0.5µl of 100µM stock CC16S-R primer, 0.5µl of 100µM stock CC16S-Probe, 5.0µl of genomic DNA, and 18.5µl of sterile H₂O. Real-time PCR was performed using the iCycler iQ Real-Time PCR Detection System (Bio-Rad, Hercules, CA). PCR conditions were as follows: 35-40 cycles of 95°C denaturation for 30 s and 55°C annealing for 30 s. The optical module was set to capture light during the annealing step. Results were analyzed using the iCycler iQ Optical System Software Version 3.0a (Bio-Rad, Hercules, CA).

Primer and probe design. Sequence alignments of the 16s rDNA sequences for strains 49025, 29029, and 43030 were constructed with ClustalV using MegAlign 5.01 (DNASTAR, Madison, WI). A sequence alignment of the 16S rDNA sequences was then performed for the following organisms: sequenced *Alicyclobacillus* strains ATCC 49025, 49029, and 43030, *A. acidoterrestris* strain DSM 3923 (AB042058), *A. cycloheptanicus* strain DSM 4006 (AB042059), *A. acidocaldarius* strain DSM 454 (AB059664), *Geobacillus subterraneus* strain K (AF276307), *Sulfobacillus disulfidooxidans* SD-11 (U34974), *B. thermoleovorans* strain ATCC 43513 (M77488), and *Clostridium elmenteitii* isolate E2SE1-B (AJ271453). The alignment was constructed with ClustalV using MegAlign 5.01 (DNASTAR, Madison, WI). Aligned regions were carefully scanned by eye to find areas of perfect identity within the representative

Alicyclobacillus species in order to create PCR priming regions. The following criteria were used for primer and probe selection: (1) 100% identity between representative sequences, (2) priming region of less than 200 bp, (3) T_m greater than 55°C, (4) C or G in the terminal positions of both 5' and 3' ends, (5) greater than 45% C+G content, and (6) no visual hairpin loops or secondary structures, confirmed using the Oligo Toolkit (Qiagen, Valencia, CA) (22).

Specificity and sensitivity tests. Assays were performed using the aforementioned PCR conditions to test for specificity of the system for *Alicyclobacillus* spp. and any cross-reactions with other common food-borne microorganisms. Genomic DNA was extracted from broth cultures of 2% *A. acidoterrestris*, *A. acidocaldarius*, and *A. cycloheptanicus* grown for 48 h at 47°C using the previously discussed DNA extraction protocol. In addition, genomic DNA was extracted from *Escherichia coli* DH-5 α , *Lactococcus lactis* subsp. *lactis*, *Geobacillus stearothermophilus* ATCC 10149 and *Pseudomonas putida* 49L/51 to test specificity of the primers and probe.

Assays for the sensitivity of the real-time PCR assay for detection of *Alicyclobacillus* were performed using tenfold serial dilutions of 10^0 to 10^{-8} of *A. acidoterrestris* in a 10 ml solution of 0.85% NaCl. Two percent cultures were initially grown for 48 h at 47°C in order to obtain an OD₆₀₀ range between 0.400 and 0.800. After dilution, cells from 1ml of each sample were collected by centrifugation at 12,000 rpm for 10 minutes for DNA extraction. Fifty microliter (50 μ l) reaction mixtures containing 0.5 μ l of CC16S-F primer, 0.5 μ l CC16S-R primer, 0.5 μ l CC16S-Probe, 33.3 μ l of sterile H₂O, 5.0 μ l of genomic DNA, 5 μ l of 10X reaction buffer, 3 μ l of MgCl₂, 2 μ l of dNTP's, and 0.2 μ l of Taq polymerase (Invitrogen, Carlsbad, CA) were used for each strain, as described above. Real-time PCR was carried out with the following cycling conditions: 35-40 cycles of 95°C and 55°C, for 30 s each. After amplification, results were analyzed using the iCycler iQ Optical System Software Version 3.0a (Bio-Rad, Hercules, CA). A range of dilutions between 10^{-3} and 10^{-7} were plated on BBL Orange Serum Agar (Difco, Detroit) for colony counting. Plates were incubated at 47°C for 48h. Additionally, sensitivity tests were performed in the same manner using apple and orange juice. Also, 1ml of culture was spiked in 9ml of Powerade sports drinks and Minute Maid Lemonade to check for any inhibitory characteristics these drinks may display in a PCR assay.

Amplification, cloning, transformation, and sequencing of 16s rDNA gene. PCR was used to successfully amplify regions of 16s rDNA from *A. acidoterrestris*, *A. acidocaldarius*, and *A. cycloheptanicus* using the 8F and 1492R primers. The Invitrogen TA cloning kit was used to insert the amplified 16s rDNA segment of each strain into pCR 2.1 vectors, and subsequently transformed into *E. coli* competent cells. Purified samples were then sent to the Plant-Microbe

Genomic Facility at the Ohio State University and sequenced using an ABI PRISM 3700 DNA Analyzer (Applied Biosystems, Foster City, CA).

TABLE V. Oligonucleotide data for *Alicyclobacillus* spp. CC16S probe and primers.

Name	Sequence	Length	T_m	G+C content
CC16S-F	CGTAGTTCGGATTGCAGGC	19 bp	65.6°C	57.9%
CC16S-R	GTGTTGCCGACTCTCGTG	18 bp	63.3°C	61.1%
CC16S-Probe	CGGAATTGCTAGTAATCGC	19 bp	57.9°C	47.4%

- 5 Development of CC16S primers and probe. Sequence data obtained from the Plant-Microbe Genomics Facility was compiled and entered into the NCBI BLAST network to check sequence integrity. Sequence data for each strain corroborated with respective sequence data in the GenBank. The 16S rDNA sequences from the three sequenced strains, as well as from *A. acidoterrestris* strain DSM 3923 (AB042058), *A. cycloheptanicus* strain DSM 4006 (AB042059),
- 10 and *A. acidocaldarius* strain DSM 454 (AB059664) were used as positive controls in the alignment to determine a suitable priming region. *B. thermoleovorans* strain ATCC 43513 (M77488) and *Clostridium elmenteitii* isolate E2SE1-B (AJ271453) were used as negative controls in the alignment. In addition, closely related *Geobacillus subterraneus* strain K (AF276307) and *Sulfobacillus disulfidooxidans* SD-11 (U34974) were added to the alignment.
- 15 Using the criteria described in the methodology, a forward and reverse primer and fluorogenic probe were derived, named CC16S-F, CC16S-R, and CC16S-Probe respectively. The sequences for the oligonucleotides are shown in Table V. This oligonucleotide set will amplify a 134 bp segment of the 16S rDNA. The alignment of the 134 bp priming region is shown in Figure 22, with the selected primer and probe oligonucleotide sequences boxed around the *Alicyclobacillus*
- 20 strains. These sequences were entered into the BLAST search network in order to discover identities with other unrelated organisms to ensure their specificity for *Alicyclobacillus*. Results show that the priming sequences are specific for 16S rDNA sequences of the three *Alicyclobacillus* species sequenced. In addition, the priming sequences also match the newly discovered species *A. hesperidum*, *A. herbarius*, *A. acidiphilus*, and *A. sendaiensis*. Also, it was
- 25 found after alignment and BLAST searches that the priming region was highly similar to the members of the *Geobacillus* and *Sulfobacillus* genera, two closely related groups. Primers CC16S-F and CC16S-R were ordered from Sigma-Genosys (The Woodlands, TX), and the CC16S-Probe was ordered from Biosearch Technologies (Novato, CA). CC16S-Probe was labeled with the reporter dye Quasar 670 on the 5' end, and quencher dye BHQ-2 on the 3' end.

Real-time PCR specificity assay. Real-Time PCR is a new method has been developed to overcome the problems of standard PCR while increasing sensitivity and allowing for nearly instantaneous results. Real-time PCR adds an optical module and a fluorogenic probe to a standard PCR assay, while including computer-based data analysis software for real-time monitoring. Real-time PCR eliminates the need for post-amplification analysis and is not affected by non-specific amplification. The optical module attached to the thermal cycler detects a fluorescent signal that is emitted from the labeled probe at each cycle during the annealing stage. The amount of emission is recorded by computer software and plotted as an exponential curve, displaying the cycle at which a significant amount of amplification takes place.

The fluorescent reporter dye is held on the 5' end of an oligonucleotide probe, with a quenching dye on the 3' end to capture fluorescence not related to amplification. When the probe anneals within the primed region, the 5' exonuclease activity of the polymerase in the reaction system cleaves the probe, inhibiting the quencher dye and increasing the emitted fluorescence from the 5' reporter dye (21).

A real-time PCR assay was developed to test the specificity of the primers and probe for *A. acidoterrestris*, *A. acidocaldarius*, and *A. cycloheptanicus*. The assay also included *E. coli* DH-5 α , *L. lactis* subsp. *lactis*, and *P. putida* to test for any unwanted cross-reactions with common foodborne microorganisms. In addition, *Geobacillus stearothermophilus* ATCC 10149 was included in the assay since it is a closely related thermophile of the *Bacillus* subfamilies. Assays were performed in triplicate, and results analyzed using the iCycler iQ Optical System Software. The results show that the reaction is specific for the three *Alicyclobacillus* while not reacting with *E. coli* DH-5 α , *L. lactis* subsp. *lactis*, or *P. putida*. However, *G. stearothermophilus* had a positive reaction within the system.

Real-time PCR sensitivity assay and limit of detection. After establishing system specificity, sensitivity of detection was determined. In order to accomplish this, tenfold serial dilutions in a 0.85% NaCl solution were made using *A. acidoterrestris* ATCC 49025 cultures. Real-time PCR assays were run in triplicate and results were analyzed using the iCycler iQ Optical System Software. A typical result is shown in Figure 23. Quantification of the lowest detection level was performed through colony counting of plated dilutions used in the PCR. Colonies were counted on OSA plates and then averaged. The CFU/ml was calculated, and cell counts were determined for the lowest positive curve by multiplying the CFU/ml by the dilution factor of the curve. Data for cell counts and detection limits is presented in Table VI. In Figure 24, the lowest accurate curve presented is from a 10⁻⁵ dilution, which is equivalent to 160 CFU/ml by plate

count. Sensitivity tests were performed in triplicate, with the limit of detection ranging between 66 and 160 cells. The mean detection limit is 103 cells.

TABLE VI. *A. acidoterrestris* cell counts and corresponding detection limits for sensitivity tests performed in saline solution and orange juice.

Replicate	Media	Mean number of colonies ^a	Mean cell count per replicate (CFU/ml)	Minimum PCR detection level per replicate ^c	Mean PCR detection level for trial set ^d
1	Saline	8	8.3×10^6 ^b	8.3×10^1	Saline solution
2	Saline	160	1.60×10^7	1.60×10^2	
3	Saline	66	6.6×10^6	6.6×10^1	
1	Orange Juice	21	2.1×10^7	2.1×10^1	Orange juice
2	Orange Juice	63	6.3×10^7	6.3×10^1	
3	Orange Juice	76	7.6×10^7	7.6×10^1	

^a Diluted samples of *A. acidoterrestris* in respective media were plated on replicate plates of BBL Orange Serum Agar (Difco, Detroit), and colony counts and averages were obtained after 48h at 47°C.

^b Calculation is estimated because no plates with between 20 and 200 colonies were available.

^c Minimum detection level is calculated by multiplying the mean cell count per replicate by the dilution level of lowest positive real-time PCR detection curve from the corresponding amplification run.

^d This is the calculated average detection limit for repeated real-time PCR trials in each type of media.

The detection limit of the *Alicyclobacillus* real-time PCR rapid screening system was also established in beverages using orange juice as a diluent. Serial dilutions were performed as previously described with juice in place of 0.85% NaCl. Juice samples were initially run in parallel with samples in 0.85% NaCl, and C_T values and curve intensities were found to be comparable in both systems. Results for the assay in orange juice are shown in Figure 25. Colony counting was performed on plated dilutions used in the PCR in order to determine cell counts at the minimum detection level. Data for cell counts and detection limits is presented in Table VI. In Figure 25, the lowest accurate curve presented is from a 10^{-6} dilution, which is equivalent to 63 CFU/ml. Sensitivity tests were performed in triplicate, with the limit of detection ranging between 21 and 76 cells. The mean detection limit is 54 cells.

The efficiency of the system has also been tested in other beverages including apple juice, three sports drinks and Lemonade purchased from local grocery stores. These beverages were spiked with *A. acidoterrestris* cultures followed by cell collection, DNA extraction and real-time

PCR detection. In all these cases, expected PCR amplification results were obtained indicating no particular inhibition by the ingredients from these tested beverages.

Discussion

A specific and sensitive real-time PCR-based rapid detection system for *Alicyclobacillus* has been developed. In the past, PCR based assays have been used to detect microorganisms in different environments (16, 2, 17, 18, 19, 20, 28). More recently, the use of real-time PCR has been a favorable alternative to standard PCR based assays due to the increased speed and sensitivity of the results, the ability to quantify detection levels, and the elimination of post-amplification analysis (21). The present method was developed by targeting the 16s rDNA gene of *Alicyclobacilli*, using *A. acidoterrestris*, *A. acidocaldarius*, and *A. cycloheptanicus* as models for primer and probe development. However, the developed primers and probe could also be beneficial in detecting newly classified members of *Alicyclobacillus*, due to high sequence identity as shown by the BLAST data. This real-time PCR assay is an improvement over traditional culture methods of detection and PCR based detection systems. Culture methods can take between three and seven days for results to be available (12, 13). While accurate, the time frame is much too long for practical industry implementation. PCR assays provide much quicker results, but false positives can be easily detected (21), and gel electrophoresis analysis must be performed after amplification. Real-time PCR assays can be readily implemented in the industry because of the real-time results. Samples can be taken from the floor as they are produced and the presence of *Alicyclobacilli* can be detected within 3 hours.

In this study, the developed primers and probes were able to specifically detect *A. acidoterrestris*, *A. acidocaldarius*, and *A. cycloheptanicus* without cross-reaction with other common foodborne microorganisms. In addition, the system could also detect the presence of *G. stearothermophilus*.

Example 2:

A real-time PCR based rapid system was developed for detecting spoilage *Alicyclobacillus* spp. in foods. A common gene of *Alicyclobacillus* spp. encoding squalene-hopene cyclase, a key enzyme involved in hopanoid biosynthesis, was targeted for specific primers and probe development. Using the combination of the primers and probe, specific detection of the presence of representative strains from *Alicyclobacillus* spp. was achieved in the Taqman-based real-time PCR assay without cross-reacting with other food-borne bacteria. The presence of around 100 cells in collected samples can be detected within several hours.

Food spoilage causes significant financial loss to the industry. Every year, about 10% of our food supplies are lost due to spoilage and a significant portion of the problem is because of

the presence of spoilage microbial agents, particularly molds, yeasts, and bacteria capable of surviving moderate heat- and acidic-treatments. Due to the limitation of applying extreme processing conditions, which can significantly alter the physiochemical properties and nutritional values of many food products, proper detection screening for the presence of microbial spoilage agents in food becomes a prior choice for quality control in the food industry. However, conventional industry practices for microbial detection from plate counting to biochemical analysis take anywhere from 48 hours to a couple of weeks. These methods are especially unsuitable for products with limited shelf life such as fruit juices. Novel detection approaches enabling rapid and specific detection of spoilage microorganisms within hours are preferred.

While the polymerase chain reaction (PCR) has been used extensively for years to rapidly amplify targeted DNA sequence regions, certain shortcomings limit its application in diagnostics and detection. For instance, PCR product analysis must be carried out after amplification, giving rise to an issue of post-amplification contamination and carry-over contamination (Heid et al., 1996). Most importantly, a high ratio of false positive results are often associated with PCR due to non-specific binding of the primers and the subsequent non-specific amplification of products. Recently a real-time PCR technology has emerged as a powerful diagnostic tool in both medical and agricultural fields.

Using real-time PCR, a fluorescent dye such as SYBR green can be incorporated into the reaction mixture and the fluorescent signals, generated from fluorescent dye binding to double stranded DNA products, can be detected directly by the optical module coupled with the thermocycler. The signals are processed by computer data analysis software for almost real-time calculation and on screen plotting. A new dimension of real-time PCR called Taqman assay further introduced a third oligonucleotide probe, labeled with 5' fluorescent reporter dye and 3' quenching dye, for signal detection (Livak et al., 1995; Basseler et al., 1995). In the Taqman system, the quenching dye on the 3' end captures the fluorescence from the 5' reporter dye so the intact probe itself does not produce strong signal. During amplification when the probe hybridized to complementary sequence within the amplified products, the 5'→3' exonuclease activity of the polymerase in the reaction system cleaves the probe, minimized the quenching effect and the emitted fluorescent signal from the 5' reporter dye can be detected by the optical module. An advantage of applying the Taqman system is that a double complementing sequence selection mechanism by both the primers and the probe is involved, therefore the false positive rate of the detection can be significantly cut down. So far, various Taqman real-time PCR-based detection approaches have been reported. However, reports on its application in the real food system are still limited. The greatest challenges are (i) effective extraction of DNA and RNA

from a system where microorganisms are mixed with the food matrix including bulk proteins, carbohydrates and fatty acids, (ii) selection of primer-and-probe sets that are specific for the target microorganisms and do not interaction with background microflora and food ingredients, and (iii) minimizing the influence of food ingredients and other chemical compounds in the food matrix on the action of enzymes involved in DNA extraction and amplification.

Our objective was to demonstrate the feasibility of the real-time PCR based detection technology for food industry applications. It is our understanding that due to the complication of various food systems, detection procedures likely need to be optimized for individual food commodities. In this study, we investigated the practicability of using the Taqman-based real-time PCR approach in detecting target microorganisms in juice products. Here we report the effectiveness of the Taqman-based detection system in rapid, specific and sensitive detection of spoilage *A. acidocaldarius* and *A. acidoterrestris* in juice products, using a primer-and-probe set specific for the *shc* gene encoding squalene-hopene cyclase.

Materials and Methods

Bacterial strains and growth conditions.

The bacterial strains used in the study and their growth conditions were listed in Table VI. ATCC 573 medium consists of 1.3g (NH₄)₂SO₄, 0.37g KH₂PO₄, 0.25g MgSO₄·7H₂O, 0.07g CaCl₂·2H₂O, 1.0g glucose, 1.0g yeast extract, and 1.0 L distilled H₂O, pH 4.0. BAM-SM ATCC 1656 medium consists of 0.25g CaCl₂·2H₂O, 0.5g MgSO₄·7H₂O, 0.2g (NH₄)₂SO₄, 3.0g KH₂PO₄, 6.0g yeast extract, 5.0g glucose, 1.0mL trace elements (0.66g CaCl₂·2H₂O, 0.18g ZnSO₄·7H₂O, 0.16g CuSO₄·5H₂O, 0.15g MnSO₄·4H₂O, 0.18g CoCl₂·6H₂O, 0.10g H₃BO₃, 0.30g Na₂MoO₄·2H₂O, 1.0L distilled H₂O), and 1.0L distilled H₂O. *Geobacillus stearothermophilus* ATCC 10149 was grown in Nutrient broth (Difco). Stock cultures of all strains were stored in their respective media plus 40% glycerol and kept at -80°C. All inoculations used were 2% concentrations made from frozen cultures.

Table VII. Bacteria cultures used in the study.

Strains	Medium and Growth Condition	Resource
<i>A. acidocaldarius</i> ATCC43030	#573 broth ^a at 48°C	ATCC
<i>A. acidoterrestris</i> ATCC49025	#1655 broth ^a at 48°C	ATCC
<i>A. cycloheptanicus</i> ATCC49029	#1656 broth ^a at 48°C	ATCC
<i>Bacillus subtilis</i>	Nutrient broth ^b , 40°C	
<i>Geobacillus</i> ?		
<i>E. coli</i> DH5α	LB broth, Miller ^c at 37°C	
<i>Pseudomonas putidis</i> ?	LB broth, Miller at 37°C	
<i>Listeria monocytogenes</i> V7	Tryptic soy broth ^d at 37°C	
<i>Lactococcus lactis</i> 2301	M17 broth ^e at 37°C	

^aAll numbered broth for *Alicyclobacillus* spp. are ATCC media.

^bFrom Becton Dickison & Co., Sparks, MD.

5 ^cFrom Fisher Chem., Fais Lawn, NJ.

^dFrom Becton Dickison and Company, Sparks, MD.

^eFrom Becton Dickison and Company, Sparks, MD.

DNA extraction, gene cloning and DNA sequencing.

For DNA extraction, cells were collected from 1 ml of bacterial culture by micro-centrifugation 7.6K rpm for 10 min. The cell
10 pellet was treated with 20 mg/ml of lysozyme (Sigma Chemical CO. St Louis, MO 63178, USA) in buffer for 45 min at 37°C. Genomic DNA was extracted using the DNeasy ® Tissue Kit (QIAGEN GmbH, D-40734 Hilden, Germany) and eluted into 100 µl of elution buffer following the instructions from the manufacturer.

The *shc* gene fragment from each strain was obtained by conventional PCR amplification
15 using degenerate primers derived from conserved amino acid sequences and the genomic DNA from each strain as template. The reaction mixture includes 1X PCR buffer, 3mM MgCl₂, 4mM dNTP (Invitrogen, Carlsbad, CA), 1µM primer pairs, 1µl of genomic DNA template and ddH₂O in a total final volume of 50µl. PCR was performed one cycle at 95°C for 3min, followed by 30 cycles at 95°C for 30s, 50°C for 30s and 72°C for 1min, with a final extension at 72°C for 7min
20 using I-cycler (Bio-Rad, Hercules, CA). PCR products were purified using the QIAquick PCR purification kit (Qiagen, Valencia, CA) following manufacturer's instruction. Purified PCR products were cloned into pCR 2.1 vectors and transformed into One Shot competent *Escherichia coli* cells using the TA Cloning kit (Invitrogen, Carlsbad, CA). Recombinant plasmids were recovered using QIAGEN miniprep (QIAGEN GmbH, D-40734 Hilden, Germany). DNA
25 sequences were determined using the ABI PRISM® 3700 DNA Analyzer (Applied Biosystems, Foster City, CA) at the Plant Genome Sequence Facility, The Ohio State University.

Real-time Taqman PCR conditions

For real-time PCR, the reaction was conducted in thin-wall microcentrifuge tubes including 1X iQ™ Supermix (Bio-Rad, Hercules, CA), 0.5 µM of primer pair, 0.3µM of probe, 10µl of genomic DNA extraction and ddH₂O in a final volume of 50µl.
30 PCR was performed one cycle at 95°C for 3min followed by 40 cycles of 95°C for 30s, 55°C for 1min using I-cycler (Bio-Rad, Hercules, CA).

DNA sequence analysis.

The DNASTAR (DNASTAR, Madison, WI) software package was used in DNA and protein sequence alignment and homology search. DNA oligonucleotide primer and probe sequences were also compared with sequences from the GenBank sequence database
35 using BlastSearch.

Specificity and sensitivity analyses Assays were conducted to test the specificity of the detection system against spoilage *Alicyclobacillus* spp. and other common food-borne microorganisms. Genomic DNA was extracted from broth cultures of *A. acidoterrestris* and *A. acidocaldarius*, grown for 48 h at 48°C (absorbance at OD₆₀₀ around 0.5-0.7), using the previously discussed DNA extraction protocol. Genomic DNAs extracted from 1 ml of overnight culture of *Escherichia coli* DH-5α, *Lactococcus lactis* subsp. *lactis* C2, *Geobacillus stearothermophilus* ATCC 10149 and *Pseudomonas putida* 49L/51 were also used in the specificity study. Ten micro liters out of the 100 micro liter of elution was used as template and the real-time PCR amplification was carried out using conditions described above but using 32 instead of 40 cycles of amplification.

The sensitivity tests of the real-time PCR assay for detection of *Alicyclobacillus* in bacterial culture media were performed using tenfold serial dilutions from 10⁰ to 10⁻⁸ of *A. acidoterrestris* in a 10ml solution of 0.85% NaCl. The initial cultures were obtained by grown for 18 h at 48°C using 2% inoculation from the frozen stock, with the absorbance reading at OD₆₀₀ range between 0.38 and 0.42. After serial dilution, cells from 1ml of each sample were collected by centrifugation at 7600 rpm for 10 minutes for DNA extraction. Ten microliter out of the 100 microliter of elution was used as template and the real-time PCR amplification was carried out as described above.

Sensitivity tests in juice products were also performed in the same manner but the serial dilutions were carried in apple juice instead of saline.

In both sensitivity analyses, a range of dilutions between 10⁻⁴ and 10⁻⁵ were plated on acidified PDA agar (Difco, Detroit) for colony counting to compare with the results by Taqman real-time PCR. Plates were incubated at 48°C for 48h.

Results

1. The primer-and-probe set used in the real-time PCR Taqman assay.

Hopanoids are membrane components involved in maintaining membrane fluidity and stability (4) of *Alicyclobacillus* spp. in extreme environmental conditions. We have targeted the *shc* gene encoding squalene-hopene cyclase, a key enzyme in hopanoid biosynthesis, for PCR primer-and-probe development.

Using an established approach (Wang et al., 2001), squalene-hopene cyclase protein sequences from several microorganisms were aligned and conserved amino acid sequences in squalene-hopene cyclase were identified. Figures 5 and 6, respectively, show the polynucleotide and protein alignments for two strains of *Alicyclobacillus*. Two degenerate primers 5' GGNGGNTGGATGTTYCARGC 3' (Y=C+T; R=A+G; N=A+T+C+G) (SEQ ID NO 64) and 5'

YTCNCCCCANCCNCCRTC 3' (SEQ ID NO 65) were derived. Using this set of primers and the genomic DNA from *A. acidocaldarius* ATCC 43030 and *A. acidoterrestris* ATCC 49025, the 705 bp *shc* fragments were amplified by PCR from both strains. The PCR fragments were cloned into the TA vector and the inserted DNA sequences were determined. The DNA sequences were further compared with other *Alicyclobacillus* spp. *shc* sequences in the GenBank. Three conserved oligonucleotides were derived including the Forward Primer 5' ATGCAGAGYTCGAACG 3' (SEQ ID NO 25) and the Reverse Primer 5' AAGCTGCCGAARCACTC 3' (SEQ ID NO 27) flanking a 136 bp fragment, and the Probe 5'TCRGARGACGTCACCGC3' (SEQ ID NO 26). The synthesized primers were ordered from Sigma-Genosys (The Woodlands, TX). The Probe is fluorescence-labeled with 5' 6-FAM BHQ-1 3' by Biosearch Technologies, Inc. (Novato, CA) and was used in the Taqman assay.

Specific detection of spoilage *Alicyclobacillus* spp.

Real-time PCR assays were performed to determine the specificity of the primers and probe for spoilage *Alicyclobacillus* spp. *E. coli* DH-5 α , *L. lactis* subsp. *lactis* C2, and *P. putida* 49L/51, *G. stearothermophilus* ATCC 10149 were also included in the study to test the possibility of cross-reactions by the primer-and-probe set with common food-borne microorganisms. Assays were performed in triplicate, and a representative real-time PCR curve plotted by the iCycler iQ Optical System Software is shown in Figure 26.

Representative strains from *A. acidocaldarius* and *A. acidoterrestris* were tested positive. No cross-reaction was detected in other commonly found food-borne microorganisms. Further specificity study was conducted by searching the Blast databases for DNA sequences from the National Center for Biotechnology Information (NCBI). We found no combination of the above three oligonucleotides in other microorganisms but *A. acidocaldarius* and *A. acidoterrestris*. The data suggested that the system is specific for spoilage *A. acidocaldarius* and *A. acidoterrestris*.

Levels of detection in bacterial culture medium and in apple juice.

To establish the detection level using the above real-time PCR system, we have conducted 10^0 to 10^{-6} serial dilutions of *A. acidoterrestris* ATCC 49025 in culture medium. Cells from 1 ml of diluted samples were collected and 10/100 of the DNAs extracted were used as template in the real-time PCR analysis. All experiments were repeated for at least three times and a representative curve was presented as Figure 27. Our results showed that using the above primer-and-probe set, the presence of as few as 10 cells in a sample could be detected. This detection level is comparable to results from other microbial detection studies using real-time PCR.

To further verify the feasibility of using the detection system in juice products, we have conducted 10^0 to 10^{-6} serial dilutions of *A. acidoterrestris* ATCC 49025 in apple juice. The experiments were repeated for three times and a representative curve was presented as Figure 28. Similar detection level was achieved in apple juice.

2. Discussion and Conclusion

Rapid, specific and sensitive detection of microorganisms in agricultural and food systems has proved to be a challenge. There are several major hurdles for effective microbial detection in the food systems. First, problematic food is normally associated with low level of initial contamination. However, the rich food matrix can support the growth of microbial agents in many cases during food storage and distribution. Thus even low level of initial contamination can cause serious damage. To be able to detect the presence of this low level contamination from food matrix often involving bulk proteins, carbohydrates and fatty acids, proper sampling and lengthy pre-detection enrichment steps are often required. To achieve rapid detection, pre-detection enrichment procedures need to be minimized and the detection system also should be sensitive enough to pick up low level of contamination.

Second, both foods and farm environment are complex ecosystems with significant background microflora. In addition to the background microflora normally associated with raw materials, beneficial microorganisms such as starter cultures sometimes are intentionally inoculated and present in large quantity in certain products. Therefore, to avoid false positive results, detection method for spoilage or pathogenic organisms needs to be specific enough to pick up only the target microorganisms. Finally, the rich and complex food ingredients often include various salts, carbohydrates, preservatives, emulsifiers, fatty acids, and proteins. The presence of these components varies among food commodities and can interfere with detection in various degrees. Therefore detection approaches and procedures need to be verified for effectiveness in these food systems.

Real-time Taqman PCR-based approach has the potential to achieve rapid, sensitive and specific detection. An average DNA amplification cycle for a small fragment can be completed within a minute. Theoretically after 30-40 cycles the amplification products from one DNA template in the system can be readily detected and plotted on the screen in almost real-time. The double sequence selection mechanism involving both the oligonucleotide primers and probe further minimizes the possibility of false positive results and enhances the detection specificity.

In this study, using a primer-and-probe set targeting the spoilage *A. acidocaldarius* and *A. acidoterrestris*, we were able to achieve specific detection without cross-reacting with representative strains from other common food-borne microorganisms including a strain from the

closely related thermophilic *G. stearothermophilus*. Although only a few representative strains were used in the laboratory specificity studies, a computer-based search covering all the world-wide deposited DNA sequences available through the NCBI website was conducted to ensure that the combination of the sequences of the oligonucleotide primers and probe used in the study are distinctive enough to detect only *A. acidocaldarius* and *A. acidoterrestris* strains.

The level of detection limit with confidence is important for any detection approaches. In this study we have conducted sensitivity tests in both bacterial cultural medium and a real food system-apple juice. For laboratory handling purpose and for the convenient of using commercially available yet economically feasible DNA extraction kit, bacterial cells were serially diluted in either medium or juice and cells in 1 ml of samples were collected by micro-centrifugation. DNA were extracted and 10/100 of the elution were used as template in PCR. The experiment was repeated at least three times and a representative curve presented as Figure 27. The lowest detection limit was determined based on the cell count numbers from agar plates derived from dilution with the optimal counting numbers (30-300) and the fold of dilution corresponding to each positive curves presented. Using this approach, we report that the presence of as few as 10 cells per sample with confidence. Because during each independent repeats the 10-fold serial dilutions were conducted without knowing exactly how many cells were in 1 ml of samples, the standard deviation reflects this fact. To further narrow down the range of standard deviation of detection, serial dilutions within the range of 2-10 can be conducted so a more precise confident level can be possibly established. We did not extrapolate the results using In other referred paper sometimes a standard curve was established first for sensitivity analysis. Furthermore, in a quality control laboratory, a regular sample size is normally 25 ml instead of 1 ml. Theoretically, sample detection limits can further be improved as long as cells from 25 ml or even 100 ml of samples can be properly collected and re-suspended in 1 ml of solution to conduct DNA extraction.

We are in the process of establishing a rapid detection system for food industry applications (the CleanPlant system) and the real-time Taqman PCR is one of our preferred platforms. In order to apply this detection platform in juice related products, we need to establish the feasibility of using the system for raw material screening and final product monitoring. We have conducted the sensitivity test by spiking the Alicyclobacillus in apple juice purchased from local grocery stores and similar level of detection was achieved indicating the applicability of such a system in final product screening. Further, we have used this system to detect the presence of Alicyclobacillus in apple juice concentrates, which are considered raw materials for the processing facilities. Similar level of detection was achieved except diluting and rinsing

procedures need to be incorporated to minimize inhibitory effects by the concentrated food ingredients (data not shown). These data suggested that

Because the system we developed is based on recognition of the signature DNA sequence of microorganisms, it has high specificity and does not cross react with other food-borne microorganisms (Figure 26). The detection limit was achieved in both bacterial culture medium and apple juice. Since no inhibition to the reaction system was detected using samples collected from apple juice, we expect the sensitivity of the detection system can be further improved by including a pre-treatment procedure to apply a centrifugation or membrane filtration procedure to concentrate the bacteria cells from a large sample volume. This approach is in fact a preferred practice in the industry where the sampling size varies from 25 ml to 1 liter. Since only 1/10 of the DNA extract was used in the reaction, we expect further improvement for the sensitivity can be achieved by incorporating more DNA template to the reaction system.

Example 3:

Yeast genomic DNA extraction protocol:

Innoculate yeast, overnight; Centrifuge 10,000 rpm for 10 mins; Discard supernatant, add 600 ul Sorbital buffer (1 M Sorbital, 100 mM EDTA, 14 mM B-mercaptoethanol, 30 ul 20 mg/ml lyticase) in pellet, vortex, room temperature for 30 min; Centrifuge 10,000 rpm for 5 min; Add 180 ATL (Qiagen DNAeasy kit) and 20 ul proteinase K (Qiagen DNAeasy kit) to pellet and vortex; 55°. for 1h, add 200 ul AL (Qiagen DNAeasy kit), 70°. for 10 min; 200 ul Ethanol, vortex, apply to DNeasy spin column.; centrifuge 10,000 rpm for 1 min, discard flow-through' add 500 ul Buffer AW1 (Qiagen DNAeasy kit), spin for 1 min; add 500 ul Buffer AW1 (Qiagen DNAeasy kit), spin for 3 min; add 100 ul AE buffer (Qiagen DNAeasy kit), spin for 1 min.

Mold genomic DNA extraction protocol:

Innoculate Mold in PDB; 3 days later, centrifuge 10,000 rpm for 10 min; add 500 ul Mold extraction buffer (1% CTAB, 1.4 M NaCl, 100 mM Tris, 20 mM EDTA, pH 8.0) to pellet; 100 ul glass beads, water bath sonic (55°.) for 45 min; add 50 ul Proteinase K (Qiagen DNAeasy kit) and incubate in 55° . for 1 h; Centrifuge 10,000 rpm for 5 min; Transfer the supernatant, add 500 ul AL (Qiagen DNAeasy kit), 70° . for 10 min; Add 200 ul Ethanol and pipet it into Dneasy mini column; 10,000 rpm for 1 min; Add 500 ul AW1 (Qiagen DNAeasy kit) , spin for 1 min; Add 500 ul AW2 (Qiagen DNAeasy kit), spin for 3 min; Add 100 AE buffer (Qiagen DNAeasy kit), spin for 1 min.

What is claimed is:

1. A method for detecting *Alicyclobacillus* and *Geobacillus* in a test sample, the method comprising

(a) providing an oligonucleotide set comprising:

(i) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 1327 through nucleotide position 1460 shown in Figure 1;

(ii) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 1327 through nucleotide position 1460 shown in Figure 1, said second consecutive sequence being downstream from said first consecutive sequence,; and

(ii) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 1327 through nucleotide position 1460 shown in Figure 1, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences;

(b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and

(c) determining the presence of PCR products of step (b), wherein the presence of a PCR product in the sample is indicative of contamination of the test sample by *Alicyclobacillus* or *Geobacillus* or both.

2. The method of claim 1 wherein the forward primer has a sequence selected from the group consisting of SEQ ID NO 1, SEQ ID NO 5, SEQ ID NO 9, SEQ ID NO 13, SEQ ID NO 17, and SEQ ID NO 20.

3. The method of claim 1 wherein the reverse primer has a sequence selected from the group consisting of SEQ ID NO 4, SEQ ID NO 8, SEQ ID NO 12, SEQ ID NO 16, SEQ ID NO 19, and SEQ ID NO 23.

4. The method of claim 1 wherein the probe has a sequence selected from the group consisting of SEQ ID NO 2, SEQ ID NO 3, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 11, SEQ ID NO 14, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, and SEQ ID NO 22.

5. A method for detecting *Alicyclobacillus* and *Geobacillus* in a test sample, the method comprising

(a) providing a oligonucleotide set comprising:

(i) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 334 through nucleotide position 485 shown in Figure 5;

(ii) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 334 through nucleotide position 485 shown in Figure 5, said second consecutive sequence being downstream from said first consecutive sequence;; and

(ii) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 334 through nucleotide position 485 shown in Figure 5, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences;

(b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and

(c) determining the presence of PCR products of step (b), wherein the presence of a PCR product in the sample is indicative of contamination of the test sample by *Alicyclobacillus* or *Geobacillus* or both.

6. The method of claim 5 wherein the forward primer has a sequence selected from the group consisting of SEQ ID NO 28, and SEQ ID NO 29.

7. The method of claim 5 wherein the reverse primer has a sequence selected from the group consisting of SEQ ID NO 34, SEQ ID NO 35, SEQ ID NO 36, and SEQ ID NO 37.

8. The method of claim 5 wherein the probe has a sequence selected from the group consisting of SEQ ID NO 30, SEQ ID NO 31, SEQ ID NO 32, and SEQ ID NO 33.

9. A method for detecting *Alicyclobacillus* and *Geobacillus* in a test sample, the method comprising

(a) providing a oligonucleotide set comprising:

(i) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 752 through nucleotide position 813 shown in Figure 1;

(ii) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 752 through nucleotide position 813 shown in Figure 1, said second consecutive sequence being downstream from said first consecutive sequence;; and

(ii) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 752 through nucleotide position 813 shown in Figure 1, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences;

(b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and

(c) determining the presence of PCR products of step (b), wherein the presence of a PCR product in the sample is indicative of contamination of the test sample by *Alicyclobacillus* or *Geobacillus* or both.

10. The method of claim 9 wherein the forward primer has a sequence selected from the group consisting of SEQ ID NO 38, SEQ ID NO 39, SEQ ID NO 40, SEQ ID NO 41, SEQ ID NO 42, and SEQ ID NO 43.

11. The method of claim 9 wherein the reverse primer has a sequence selected from the group consisting of SEQ ID NO 50, SEQ ID NO 51, SEQ ID NO 52, and SEQ ID NO 53.

12. The method of claim 9 wherein the probe has a sequence selected from the group consisting of SEQ ID NO 44, SEQ ID NO 45, SEQ ID NO 46, SEQ ID NO 47, SEQ ID NO 48, and SEQ ID NO 49.

13. A method for detecting mold or yeast in a test sample, the method comprising

(a) providing a oligonucleotide set comprising:

(i) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 81 through nucleotide position 225 shown in Figure 8;

(ii) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 81 through nucleotide position 225 shown in Figure 8, said second consecutive sequence being downstream from said first consecutive sequence,; and

(ii) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 81 through nucleotide position 225 shown in Figure 8, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences;

(b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and

(c) determining the presence of PCR products of step (b), wherein the presence of a PCR product in the sample is indicative of contamination of the test sample by *mold or yeast* or both.

14. The method of claim 13 wherein the forward primer has a sequence selected from the group consisting of SEQ ID NO 54, and SEQ ID NO 58.

15. The method of claim 13 wherein the reverse primer has a sequence selected from the group consisting of SEQ ID NO 55, and SEQ ID NO 59.

16. The method of claim 13 wherein the probe has a sequence selected from the group consisting of SEQ ID NO 56, SEQ ID NO 57, and SEQ ID NO 60

17. A method for detecting mold or yeast in a test sample, the method comprising

(a) providing a oligonucleotide set comprising:

(i) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 114 through nucleotide position 238 shown in Figure 8;

(ii) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 114 through nucleotide position 238 shown in Figure 8, said second consecutive sequence being downstream from said first consecutive sequence,; and

(ii) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is identical to a third consecutive sequence within the sequence of nucleotide position 114 through nucleotide position 238 shown in Figure 8, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences;

(b) amplifying DNA in the sample with the said primer set and a polymerase chain reaction, and

(c) determining the presence of PCR products of step (b), wherein the presence of a PCR product in the sample is indicative of contamination of the test sample by *mold or yeast* or both.

18. The method of claim 17 wherein the forward primer has a sequence of SEQ ID NO 61.

19. The method of claim 17 wherein the reverse primer has a sequence of SEQ ID NO 62.

20. The method of claim 17 wherein the probe has a sequence of SEQ ID NO 63.

21. The method of claim 1 wherein the primers

- i.) do not contain runs of more than 5 of the same nucleotide base,
- ii) do not contain internal palindromic sequences,
- iii) do not hybridize to one another under stringent conditions, and
- iv) have 40 to 60 percent G+C content, and

wherein said PCR amplification provides a PCR product that is from 50 to 613 nucleotides in length

22. The method of claim 1, wherein the PCR is quantitative PCR.

23. The method of claim 1, wherein the PCR is real-time PCR.

24. A method of detecting the presence of acidic bacteria in a test sample using real time monitoring of a polymerase chain reaction amplification of a target nucleic acid sequence found in the acidic bacteria, said method comprising the steps of

(a) adding to the test sample an effective amount of a forward nucleic acid primer and reverse nucleic acid primer and a nucleic acid probe, wherein the forward primer is selected from the group consisting of SEQ ID NO 1, SEQ ID NO 5, SEQ ID NO 9, SEQ ID NO 13, SEQ ID NO 17, and SEQ ID NO 20, and wherein the reverse primer is selected from the group consisting of SEQ ID NO 4, SEQ ID NO 8, SEQ ID NO 12, SEQ ID NO 16, SEQ ID NO 19, and SEQ ID NO 23, and wherein the probe is selected from the group consisting of SEQ ID NO 2, SEQ ID NO 3,

SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 10, SEQ ID NO 11, SEQ ID NO 14, SEQ ID NO 15, SEQ ID NO 18, SEQ ID NO 21, and SEQ ID NO 22 and wherein the probe hybridizes to an amplified copy of the target nucleic acid sequence, and wherein the probe is labeled with a marker which emits a signal upon the hybridization of the probe to the target nucleic acid sequence;

(b) amplifying the target nucleic acid sequence by polymerase chain reaction;

(c) detecting the emitted signal of the sample.

25. A method of detecting the presence of fungi in a test sample using real time monitoring of a polymerase chain reaction amplification of a target nucleic acid sequence found in the acidic bacteria, said method comprising the steps of

(a) adding to the test sample an effective amount of a forward nucleic acid primer and reverse nucleic acid primer and a nucleic acid probe, wherein the forward primer is selected from the group consisting of SEQ ID NO 54, and SEQ ID NO 58 and SEQ ID NO 61

, and wherein the reverse primer is selected from the group consisting of SEQ ID NO 55, SEQ ID NO 59, and SEQ ID NO 62, and wherein the probe is selected from the group consisting of SEQ ID NO 56, SEQ ID NO 57, SEQ ID NO 60, and SEQ ID NO 63 and wherein the probe hybridizes to an amplified copy of the target nucleic acid sequence, and wherein the probe is labeled with a marker which emits a signal upon the hybridization of the probe to the target nucleic acid sequence;

(b) amplifying the target nucleic acid sequence by polymerase chain reaction;

(c) detecting the emitted signal of the sample.

26. A kit for detecting *Alicyclobacillus* and *Geobacillus* in a test sample, comprising a set of oligonucleotides comprising:

(a) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 1327 through nucleotide position 1460 shown in Figure 1;

(b) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 1327 through nucleotide position 1460 shown in Figure 1, said second consecutive sequence being downstream from said first consecutive sequence; and

(c) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 1327 through nucleotide position 1460 shown in Figure 1, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences.

27. A kit for detecting *Alicyclobacillus* and *Geobacillus* in a test sample, comprising a set of oligonucleotides comprising:

(a) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 334 through nucleotide position 485 shown in Figure 5;

(b) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 334 through nucleotide position 485 shown in Figure 5, said second consecutive sequence being downstream from said first consecutive sequence; and

(c) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 334 through nucleotide position 485 shown in Figure 5, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences.

27. A kit for detecting *Alicyclobacillus* and *Geobacillus* in a test sample, comprising a set of oligonucleotides comprising:

(a) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 752 through nucleotide position 813 shown in Figure 5;

(b) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 752 through nucleotide position 813 shown in Figure 5, said second consecutive sequence being downstream from said first consecutive sequence; and

(c) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 752 through nucleotide position 813 shown in Figure 5, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences.

28. A kit for detecting *yeast or mold* in a test sample, comprising a set of oligonucleotides comprising:

(a) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 81 through nucleotide position 225 shown in Figure 8;

(b) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 81 through nucleotide position 225 shown in Figure 8, said second consecutive sequence being downstream from said first consecutive sequence; and

(c) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 81 through nucleotide position 225 shown in Figure 8, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences.

29. A kit for detecting *yeast or mold* in a test sample, comprising a set of oligonucleotides comprising:

(a) a forward primer of from 15 to 35 nucleotides in length, said forward primer comprising a sequence which is identical to a first consecutive sequence within the sequence of nucleotide position 114 through nucleotide position 238 shown in Figure 8;

(b) a reverse primer of from 15 to 35 nucleotides in length, said reverse primer comprising a sequence which is complementary to the inverse complement of a second consecutive sequence within the sequence of nucleotide position 114 through nucleotide position 238 shown in Figure 8, said second consecutive sequence being downstream from said first consecutive sequence; and

(c) a probe of from at least 15 nucleotides in length, said probe comprising a sequence which is which is identical to a third consecutive sequence within the sequence of nucleotide position 114 through nucleotide position 238 shown in Figure 8, or the complement thereof, and falls between or overlaps with the first and second consecutive sequences.

Friday, September 05, 2003 9:42 AM

.....GACGAAACGGCTGGCGGCGGTGC Consensus #1
AGAGTTTGATCCTGGCTCAGGACGAAACGGCTGGCGGCGGTGC Majority

[illegible]

CTAATACATGCAAGTCCGAGCG...CCTTCGG.GG..AGC Consensus #1
CTAATACATGCAAGTCCGAGCGG-CCCTTCGG-GGCCACGC Majority

41	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	C	G	G	T	C	T	C	T	C	G	G	A	G	G	C	C	A	G	C		
21	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	C	G	A	G	-	C	C	C	T	T	C	G	G	-	G	G	C	T	A	G	C
41	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	C	G	A	-	C	C	C	T	T	C	G	G	-	G	G	T	C	A	G	C	

GGCGGACGGGTGAG . AACACGTGGG . AATC . GCC . . C . G Consensus #1
GGCGGACGGGTGAGTAACACGTGGGTAATCTGCCCTTTCAG Majority

	90	100	110	120	
81	G G C G G A C G G G T G A G	A A C A C G T G G G T A A T C T	G C C T T T C A G	43030	16S
59	G G C G G A C G G G T G A G T A	A A C A C G T G G G G C A A T C C	T T T C A G	49025	16S
79	G G C G G A C G G G T G A G T A	A A C A C G T G G G T A A T C T	G C C C A A C T T G	49029	16S

. C . G G A A T A A C . C . . G G A A A C G G G . G C T A A . G C C G G A T A . Consensus #1
 A C C G G A A T A A C G C C C G G A A A C G G G T G C T A A T G C C G G A T A X Majority

	130	140	150	160
121	G C C G G A A T A A C G C C C G G A A A C G G G C G C T A A A G C C G G A T A C			43030 16S
99	A C T G G A A T A A C A C T C G G A A A C G G G T G C C T A A T G C C G G A T A -			49025 16S
119	A C C G G A A T A A C G C C C T G G A A A C G G G T G C C T A A T G C C G G A T A G			49029 16S

Page 2

	...	CG	G	.AGG	CA	TCT	.CT	G	...	G	.AAG	...	CAA	.T	Consensus #1				
	GCAC	GGAG	XA	GGCA	TCT	CT	CT	TTGC	GGGA	AAAG	GTGC	CA	AX	T	Majority				
		170		180		190		200											
161		G	C	C	C	G	G	A	G	A	G	G	C	C	A	A	T	43030 16s	
1138		A	T	A	C	A	C	G	G	T	A	G	G	C	A	T	C	T	49025 16s
1159		G	C	A	-	G	C	G	A	G	C	A	G	G	C	A	T	G	49029 16s
		G	...	CGC	.GA	..	GAGG	AGCC	CGCG	CGGC	ATTA	AGCT	.GTT	G	Consensus #1				
		G	C	A	T	C	G	C	T	G	A	G	A	G	A	G	C	A	Majority
			210		220		230		240										
201		G	G	G	T	C	G	C	T	G	A	G	A	G	A	G	C	T	43030 16s
1178		G	C	A	T	C	G	C	T	G	A	G	A	G	A	G	C	T	49025 16s
1198		G	C	A	C	C	G	C	A	G	A	T	G	G	A	G	C	T	49029 16s
		G	.G	.GGT	AA	C	GGC	.CA	CC	AA	AG	GC	GA	CG	AT	GC	GT	AG	Consensus #1
		G	T	G	G	G	G	T	AA	C	GGC	T	CA	CC	AA	AG	GC	GA	Majority
			250		260		270		280										
241		G	C	G	G	G	T	AA	C	GG	C	C	AA	AG	GC	GA	CG	GT	43030 16s
218		G	T	G	A	GG	T	AA	C	GG	C	T	CA	CC	AA	AG	GC	GA	49025 16s
2238		G	T	G	G	G	G	T	AA	C	GG	C	T	CA	CC	AA	AG	GC	49029 16s
		C	T	G	A	G	A	G	G	T	G	..	CGG	CC	ACA	CA	CT	GG	Consensus #1
		C	T	G	A	G	A	G	G	T	G	A	C	CGG	CC	ACA	CA	CT	Majority
			290		300		310		320										
281		C	T	G	A	G	A	G	G	T	G	A	C	CGG	CC	ACA	CA	CT	43030 16s
258		C	T	G	A	G	A	G	G	T	G	A	C	CGG	CC	ACA	CA	CT	49025 16s
278		C	T	G	A	G	A	G	G	T	G	A	C	CGG	CC	ACA	CA	CT	49029 16s

Alignment 1

Alignment Report of Unfiled ClustalV (Weighted)
Friday, September 05, 2003 9:42 AM

	C	A	G	A	C	T	C	C	T	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	A	A	T	C	T	T	C	C	G	C	A	A	Consensus #1				
	C	A	G	A	C	T	C	C	T	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	A	A	T	C	T	T	C	C	G	C	A	A	Majority				
											330											340											350											360
321	C	A	G	A	C	T	C	C	T	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	A	A	T	C	T	T	C	C	G	C	A	A	43030 16s				
298	C	A	G	A	C	T	C	C	T	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	A	A	T	C	T	T	C	C	G	C	A	A	49025 16s				
318	C	A	G	A	C	T	C	C	T	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	A	A	T	C	T	T	C	C	G	C	A	A	49029 16s				
											370											380											390											400
	T	G	G	G	C	G	C	A	A	G	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	G	T	G	A	G	C	G	A	A	G	A	Consensus #1			
	T	G	G	G	C	G	C	A	A	G	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	G	T	G	A	G	C	G	A	A	G	A	Majority			
											370											380											390											400
361	T	G	G	G	C	G	C	A	A	G	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	G	T	G	A	G	C	G	A	A	G	A	43030 16s			
338	T	G	G	G	C	G	C	A	A	G	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	G	T	G	A	G	C	G	A	A	G	A	49025 16s			
358	T	G	G	G	C	G	C	A	A	G	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	G	T	G	A	G	C	G	A	A	G	A	49029 16s			
	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	C	T	C	. G	T	. .	C	T	C	G	G	G	. A	G	A	G	C	G	Consensus #1						
	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	C	T	C	T	G	T	T	G	C	T	C	G	G	G	A	G	A	G	C	G	Majority				
											410											420											430											440
401	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	C	T	C	T	G	T	T	G	C	T	C	G	G	G	A	G	A	G	C	G	43030 16s				
378	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	A	G	C	T	C	T	G	T	T	G	C	T	C	G	G	G	A	G	A	G	C	G	49025 16s			
398	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	A	G	C	T	C	A	G	T	C	A	C	T	C	G	G	A	A	G	A	G	C	G	49029 16s			
	. C	A	. G	G	. G	. .	T	G	G	A	A	A	G	C	. C	C	. T	T	G	. G	A	C	G	G	T	A	C	C	G	A	G	. Consensus #1												
	G	C	A	A	G	G	G	A	G	T	G	G	A	A	A	G	C	C	C	T	T	G	X	G	A	G	A	C	G	G	T	A	C	C	G	A	G	T	Majority					
											450											460											470											480
441	G	C	A	T	G	G	G	G	A	T	G	G	A	A	A	G	C	C	C	G	T	G	C	G	A	C	G	G	T	A	C	C	G	A	G	T	43030 16s							
418	A	C	A	A	G	G	A	G	A	G	T	G	G	A	A	A	G	C	T	C	C	T	T	G	T	G	A	G	A	C	G	G	T	A	C	C	G	A	G	T	49025 16s			
438	G	C	A	A	G	G	G	A	G	T	G	G	A	A	A	A	G	C	C	C	T	T	G	A	G	A	C	G	G	T	A	C	C	G	A	G	A	49029 16s						

Alignment 1

Alignment Report of Unfiled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

		Consensus #1									
		Majority									
		490	500	510	520						
481	G A G G A A G C C C C G G C T A A C T A C G T G C C A G C A G C C G C G G T A A	43030 16s									
458	G A G G A A G C C C C G G C T A A C T A C G T G C C A G C A G C C G C G G T A A	49025 16s									
478	G A G G A A G C C C C G G C T A A C T A C G T G C C A G C A G C C G C G G T A A	49029 16s									
		Consensus #1									
		Majority									
		530	540	550	560						
521	A A C G T A G G G G G C G A G C G T T G T C C G G A A T C A C T G G G - C G T A	43030 16s									
498	T A C G T A G G G G G C A A G C G T T G T C C G G A A T C A C T G G G C G T A	49025 16s									
518	T A C G T A G G G G G C A A G C G T T G T C C G G A A T C A C T G G G - C G T A	49029 16s									
		Consensus #1									
		Majority									
		570	580	590	600						
560	A A G G T G C G T A G G C G G T C G A G C A A G T C T G G A A A G T C	43030 16s									
538	A A G C G T G C G T A N G C G G T T G T G T A A G T C T G A A A G T C	49025 16s									
557	A A G C G T G C G T A G G C G G T T G C G T G T G T C C G G G T G A A A G T C	49029 16s									
		Consensus #1									
		Majority									
		610	620	630	640						
600	C A T G G C T C A A C C A T G G G A T G G C T T T G G A A A C T G C T T G - A C	43030 16s									
578	C A A G G C T C N A C C T T G G G N A T G C T T T G G A A A C T G C T A T G A C	49025 16s									
597	C A G G C T C A A C C C T T G G G A A T G C C T T T G G A A A C T G C T A - A C	49029 16s									

C A . G G C T C . A C C . T G G G . . . G C . T T G G A A A C T G C . T . . A C Consensus #1
 C A X G G C T C A A C C X T G G G A A T G C T T T G G A A A A C T G C X T G - A C Majority

	650	660	670	680	Consensus #1 Majority
T T G A G T G C T G G A G A G G C . A G G . . A A T T C C . C G T G T . A . C G					
T T G A G T G C T G G A G A G G C A A G G G A A T T C C X C C G T G T - A G C G					
T T G A G T G C T G G A G A G G C A A G G G A A T T C C A C G T G T - A G C G					43030 16S
T T G A G T G C T G G A G A G G C N A A A T T C C N C G T G T A C C G					49025 16S
T T G A G T G C T G G A G A G G C A A G G G A A T T C C G C G T G T - A G C G					49029 16S
G T G . A A . T G C G . . A . A . A T G . G G A G G A A T A C C A G T G G C . A					Consensus #1
G T G X A A - T G C C G T - A G A T A T G T G G A G G A A T A C C A G T G G C G A					Majority
G T G A A A - T G C C G T - A G A T A T G T G G A G G A A T A C C A G T G G C G A					
G T G A A A - T G C C G T - A G A T A T G T G G A G G A A T A C C A G T G G C G A					43030 16S
G T G N A A A T G C C G N T A N A T A T G T G G A G G A A T A C C A G T G G C N A					49025 16S
G T G G A A - T G C C G T - A G A T A T G C G G A G G A A T A C C A G T G G C G A					49029 16S
A . G C G C C T T . G C T G G A C A G T G . A C T G A C G C T G A . G G C A C G					Consensus #1
A X G C G C C T T - G C T G G A C A G T G - A C T G A C G C T G A - G G C A C G					Majority
A R G C G C C T T - G C T G G A C A G T G - A C T G A C G C T G A - G G C A C G					43030 16S
A N G C G C C T T T G C T G G A C A G T G G A C T G A C G C T G A A G G C A C G					49025 16S
A G G C G C C T T - G C T G G A C A G T G - A C T G A C G C T G A - G G C A C G					49029 16S
A A A . . C G T G G G A . C A A .					Consensus #1
A A A - G C G T G G G G A G C A A - .					Majority
A A A - G C G T G G G G A G C A A - .					
A A A A N C G T G G G G A N C A A C N G G A T T A N A T C C C C N A A N G C G N					43030 16S
A A A - G C G T G G G G A G C A A - .					49025 16S
A A A - G C G T G G G G A G C A A - .					49029 16S

Alignment 1

	810	820	830	840	Consensus #1
769	- - - - -	A C A G G A T T A G A T . C C C . . . G T A G T C C . . C .			43030 16s
778	G G G A A G C A A	A C A G G A T T A G A T T C C C N T T G T A G T C C C G C C			49025 16s
766	- - - - -	A C A G G A T T A G A T A C C C T G - G T A G T C C - A C G			49029 16s
	850	860	870	880	Consensus #1
797	C C G T A A A C G A T G A G T G C T - A G G T G T T G G G G G G A C A C A C C C				43030 16s
818	C C G T A A A C N A T G A G T A C T T A G T T G T T G G G G G A A C A C A C C C				49025 16s
794	C C G T A A A C G A T G A G T G C T - A G G T G T T G G G G G G T A C C A C C C				49029 16s
	890	900	910	920	Consensus #1
836	- C A G T G C C G A A G G A A A M C C A A T A A G C A C T C C G C C T G G G G A				43030 16s
858	- C A N T G C - G N G G A A A C C C A A T A A G C A C T C C G C C T G G G G A				49025 16s
833	T C A G T G C C G A A G G A A A C C C A A T A A G C A C T C C G C C T G G G G A				49029 16s
	930	940	950	960	Consensus #1
875	G T A C G G T C C A A G A C T G A A . C T C A A A G G A A T T G A C G G G G G				43030 16s
896	G T G C G G T C N C A A G A C T G A A N C T C A A A G G A A T T G A C G G G G G				49025 16s
873	G T A C G G T C G C A A G A C T G A A A C T C A A A G G A A T T G A C G G G G G				49029 16s

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)
Friday, September 05, 2003 9:42 AM

C C C G C A C A A G C A G T G G A G C A T . T G G T T T A A . T C G A A G C A A Consensus #1									
C C C G C A C A A G C A G T G G A G C A T T T A A T T C G A A G C A A Majority									

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)
Friday, September 05, 2003 9:42 AM

TTT . A G T C C C G C A A C G A G C G C A A C C C T T G A . C T G T G T T A C C C o n s e n s u s # 1
T T A A G T C C C G C A A C G A G C G C A A C C C T T G A X C T G T G T T A C C M a j o r i t y

	1130	1140	1150	1160
11075	T T C A G T C C C G C A A C G A G C G C A A C C C T T G A C	C T G T G T T A C C	43030	16s
11096	T T A A G T C C C C G C A A C G A G C G C A A C C C T T G A C	C T G T G T T A C C	49025	16s
11073	T T A A G T C C C C G C A A C G A G C G C A A C C C T T G A C	C T G T G T T A C C	49029	16s

AGC . CGT . . . GG . GGGGACTCACAG . TGACTGCCGGCGTA Consensus #1
AGCACGTTGAGGTTGGGGACTCACAGGTGACTGCCGGCGTA Majority

	1170	1180	1190	1200	
1115	A G C G	C G T T G A G G	C G G G G A C T C A C A G G	T G A C T G C C G G C G T A	43030 16s
1116	A G C A C G T T G T	G G T G G G G A C T C A C A G G	T G A C T G C C G G C G T A	49025 16s	
1117	A G C A C G T G A A G G T G G G G A C T C A C A G	T T G A C T G C C G G C G T A	49029 16s		

AGTCGGAGGAAGGCGGGGATGACGTCAATACTATCATGCCC
AGTCGGAGGAAGGCGGGGATGACGTCAATACTATCATGCCC

	1210	1220	1230	1240
1155	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C	43030	168	
1176	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C	49025	168	
1153	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C	49029	168	

. T . A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C G G . A C Consensus #1
T T T A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C G G T A C Majority

	1250								1260								1270								1280																	
1195	C	T	G	A	T	G	T	C	C	T	G	G	G	C	T	A	C	A	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	43030	16S
1216	T	T	T	A	T	G	T	C	C	T	G	G	G	C	T	A	C	A	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	49025	16S
1193	T	T	T	A	T	G	T	C	C	T	G	G	G	C	T	A	C	A	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	49029	16S

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

A A . G G G A . G C G A . . C C G C G A G G . G G A G C . A A . C C . . . A A A Consensus #1		A A C G G G A A G C G A A G C C G C G A G G T G G A G C A A A C C C A A A A Majority	
1290		1300	
1235 A A G G G A G C C G A A G C C G C G A G G C G G A G C G A A C C C A A A A 43030 16s		1310	
1256 A A C G G G A A G C G A A G C C G C G A G G T G G A G C A A A C C T A A A A A 49025 16s		1320	
1233 A A C G G G A A G C G A G A C C G C G A G G T G G A G C A A A C C C T G A A A 49029 16s			
G C C G . T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A Consensus #1		G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A Majority	
1275 G C C G C T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 43030 16s		1350	
1296 G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 49025 16s		1360	
1273 G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 49029 16s			
T G A A G C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C Consensus #1		T G A A G C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C Majority	
1315 T G A A G C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 43030 16s		1390	
1336 T G A A G C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 49025 16s		1400	
1313 T G A A G C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 49029 16s			
G G T G A A T . C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C Consensus #1		G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C Majority	
1355 G G T G A A T A C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 43030 16s		1430	
1376 G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 49025 16s		1440	
1353 G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 49029 16s			

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G . G G T A A C C	Consensus #1
A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T A A C C	Majority

1395	A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C	1480	43030 16s
1416	A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C		49025 16s
1393	A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G G G T A A C C		49029 16s

. . T G G A G C C A G C C G C C G A A G G T G G G T . G A T G A T T G	Consensus #1
C X T X T X G G G A G C C A G C C G C C G A A G G T G G G T T G A T G A T T G	Majority

1435	C C T G T G G G A G C C A G C C G C C G A A G G T G G G T C G A T G A T T G	1520	43030 16s
1456	G T T A T - - G G A G C C A G C C G C C G A A G G T G G G T T G A T G A T T G		49025 16s
1433	C G T - C A G G G A G C C A G C C G C C G A A G G T G G G T T G A T G A T T G		49029 16s

G G G T G A A G T C G T A A C A A G G T A G C C G T	Consensus #1
G G G T G A A G T C G T A A C A A G G T A G C C G T	Majority

1475	G G G T G A A G T C G T A A C A A G G T A G C C G T	43030 16s
1494	G G G T G A A G T C G T A A C A A G G T A G C C G T	49025 16s
1472	G G G T G A A G T C G T A A C A A G G T A G C C G T	49029 16s

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Figure 2

Sequence, 49029 16S

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AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCCTAATAATGCAAGTCGAGCGGACCCCTTCGGGGTCAGCGG
5  CGGACGGGTGAGTAAACACGTGGGTAATCTGCCCAAACGTGACCGGAATAACGCCCTGGAAAACGGGTGCTAATGCCGGATAGGC
  AGCGAGCAGGCATCTGCTCGCTGGGAAAAGGTGCAAGTGCACCGCAGATGGAGGAGCCCCGGCGGCATTAGCTGGTTGGTG
  GGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGGACGGCCACACTGGGACTGAGACACCGGCCAG
  ACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGCAAGCCCTACCGGAGCAAACGCCCGCTGAGCGAAGAAGG
  CCTTCGGGTTGTAAAGCTCAGTCACTCGGGAAGAGCGGCAGGGGAGTGGAAAAGCCCCCTTGAGAGACGGTACCGGAGAG
10  GAAGCCCCGGCTAAC'TACGTGCCAGCAGCCCGGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGC
  GTGCGTAGGCGGTTGCGTGTCTCCGGGTGAAGTCCAGGGCTCAACCCCTGGGAATGCC'TTGGAAAAC'TGCCGTAACTTGAG
  TGCTGGAGAGGCAAGGGGAATTCCGCGTGTAGCGGTGGAATGCGTAGATA'TGCCGAGGAATA'CCAGTGGCGAAGGCGCCT
  TGCTGGACAGTGACTGACGCTGAGGCACGAAAGCGTGGGAGCAAAACAGGAT'TAGATACCCCTGGTAGTCCACGCCGTAAA
  CGATGAGTGTAGGTGTTGGGGGTACCAACCCTCAGTGCCGAAGGAAACCCAA'TAAGCACTCCGCCCTGGGGAGTACGGTC
15  GCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAAGCAGTGGAGCATGTGGTTTAA'TTCGAAGCAA'CGCGAAGA
  ACCTTANCAGGGCTCGACATCCCCCTGACAGCCGACAGATGCGGTTTCCCTTCGGGGCAGGGGAGACAGGTGGTGCATG
  GTTGTGTCGTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGCAA'CGAGCGCAAACCC'TTGAACTGTGT'TACCAGCACGTG
  AAGTGGGGACTCACAGTTGACTGCCGGCGTAAAGT'CGGAGGAAGCGGGGATGACGTCAAATCATCATGCCCTTTATGTC
  CTGGGCTACACACGTGCTACAAATGGGCGGTACAA'CGGGAAGCGAGACCGCGAGGTGGAGCAAACCCCTGAAAGCCGTTTCG
20  TAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATTGCTAGTAA'TCGCGGATCAGCATGCCCGGTTGAATC
  CGTTCGGGGCTTGTACACACCGCCCGTCA'CA'CCAGAGT'CGGCAA'CA'CCCGAAGT'CGGTGGGGTAA'CCCGTCA'GGG
  AGCCAGCCCGCCGAAGGTGGGTTGATGATTGGGGTGAAGTCGTAAACAAGGTAGCCGT

```

Figure 3

49025 16S
 5 GACGAA CGCTGGCGGCGTGCC TAAATACATGCAAGTCGAGCGAGCCCTTCGGGGCTAGCGGCGGACGGGTGAGTAACACGT 80
 GGGCAATCCGCCCTTTCAGACTGGAATAACACTCGGAAACGGGTGCTAATGCCGGATAATAACACGGGTAGGCATCTACTTG 160
 TGTGAAAGATGCAACTGCACTCGCTGAGAGAGGCCCGCGGCAATTAGCTAGTTGGTGAGGTAAACGGCTCACCAAGGC 240
 GACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAG 320
 TAGGGAATCTTCGCAATGGCGCAAGCCTGACGGAGCAACGCCCGCTGAGCGGAAGAGGCCCTTCGGGTTGTAAAGCTCT 400
 GTTGCTCGGGAGAGCGACAAGGAGAGTGGAAAGCTCTTGTGAGACGGTACCGAGTGAGGAAGCCCCGGCTAACTACGT 480
 10 GCCAGCAGCCGCGGTAAATACGTAGGGGGCAAGCGTTGTCCGGAAATCACTGGGGCGTAAAGCGTGCCTANGCGGTTGTGTA 560
 AGTCTGAACTGAAAGTCCAAGGCTCNA CCTTGGGNATGCTTTGGAAACTTGCA TGGACTTGAGTGTGGAGAGGCNAGGCN 640
 AATTCCNCGTGTACCGGTGNA AATGCCNTANATATGTGGAGGAA TACCAGTGGCNAANGCCCTTTGCTGGACAGTGGGA 720
 CTGACGCTGAAGGCACGAAANCGTGGGGANCAACNGGATTANATCCCCNAANGCGNGGGGAAGCAAAACAGGATTAGATT 800
 CCCNTTGTAGTCCCGCCCCCGTAANCNATGAGTACTTAGTTGTTGGGGAAACACACCCCAN TGCGNGGAAACCCAAATAAG 880
 15 CACTCCGCCCTGGGGAGTGGGTCNCAAGACTGAANCTCAAAGGAATTGACGGGGGCCCGCAACAAGCAGTGGAGCATNTGG 960
 TTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGGCTNGACATCCCCTGACCGGTGCAGAGATGTACCTTCCCTTCGGG 1040
 GCAGAGGACACAGGTGGTGCA TGGTTGTCTCGTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCC 1120
 TTGATCTGTGTTACCAAGCAGTGTGTGGGGA CTCAAGGTGACTGCCGGCGTAAAGTCCGAGGAAGCGGGGGATGACGT 1200
 CAAATCATCATGCCCTTTATGTCCTGGGCTACACACGTGCTACAAATGGGCGGTACAAACGGGAAGCGAAAGCCGCGAGGTGG 1280
 20 AGCAAAACCTTAAAGCCGTTCTGATGTTCCGATGCAAGTGCCTGCAATGAAGCCGGAATTGCTAGTAATCGC 1360
 GGATCAGCATGCCGCGGTGAATCCGTTCCCGGGCCTTGTAACAACCGCCCGTCAACAACGAGAGTCCGGCAACACCCGAA 1440
 GTCGGTGAGGTAAACCGTTATGGAGCCAGCCCGCGAAGGTGGGTTGATGATTGGGGTGAAGTCGTAAACAAGGTAGCCGT 1519

Figure 4

43030 16S
 5 AGAGTTTGATCCTGGCTCAGGACGAAACGCTGGCGGCGTGCCCTAAATACATGCAAGTCGAGCGGGTCTCTTCGGAGGCCAGC
 GCGGACGGGTGAGGAACACGTGGGTAAATCTGCCCTTTCAGGCCGGAAATAACGCCCGGAAACGGGCGCTAAAGCCGGATAC
 GCCCGAGAGGAGCATCTTCTTTCGGGGGAAGGCCAAATTGGGTCTGCTGAGAGAGGAGCCCGCGGCATTAGCTAGTTG
 GCGGGGTAAACGGCCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACCGGCCACACTGGGACTGAGACACGGCC
 CAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGCAAGCCTGACGGAGCAACGCCCGCTGAGCCGAAGA
 AGCCCTTCGGGTGTAAAGCTCTGTGTCTCGGGGAGAGCGGCATGGGGGATGGAAAGCCCCGTGCCGAGACGGTACCGAGT
 10 GAGGAAGCCCCCGCTAAC'TACGTGCCAGCAGCCGCGGTAAACG'TAGGGGCGAGCGTGTGTCCGGAATCAC'TGGGCGTAA
 AGGTGCGTAGGCGGTGAGCAAGTCTGGAGTGAAAGTCCATGGCTCAACCATGGGATGGCTTTGGAAACTGCTTGACTT
 GAGTGTGGAGAGGCAAGGGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCAAGTGGCGGAARGCG
 CCTTGTGGACAGTGACTGACGCTGAGGCACGAAAGCGTGGGAGCAAAACAGGATTAGATACCC'TGGTAGTCCACGCCGT
 AAACGATGAGTGTAGGTGTTGGGGGACACACCCAGTCCGAAAGGAAAMCCAAATAAGCACTCCGCC'TGGGAGTACGG
 15 TCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAAGCAGTGGAGCATGTGTTTAAATCGAAGCAACGCGAA
 GAACCTTACCAGGGCTTGACATCCC'TCTGACACCCCTCAGAGATGAGGGGTCCC'TTCGGGCGAGAGAGACAGGTGGTGCA
 TGGTTGTCTCGTCAGCTCGTTCGTGAGATGTTGGTTTCAGTCCCGCAACGAGCGCAACCC'TTGACCTGTGTACCAGCGCG
 TTGAGGCGGGGACTCACAGGTGACTGCCCGCGTAAAGTCCGAGGAAGCGGGGATGACGTCAAATCATTCATGCCCTGATG
 TCC'TGGGCTACACACGTGCTACAATGGGCGGAACAAAGGAGGCGGAAGCCCGAGGGCGGAGCGAAACCCCAAAGCCGCT
 CGTAGTTCGGATTGCAGGCTGCAACTCGCCCTGCATGAAGCCGGAATTGCTAGTAATCGCGGATCAGCATGCCCGGTGAA
 20 TACGTTCCCGGGCCTTGTAACAACCGCCCGTCAACCAAGAGTCCGGCAACAACCGAAGTCCGTGAGGTAAACCCCTGTG
 GGGAGCCAGCCCGCAAGGTGGGTGATGATTGGGTGAAGTCGTAAACAAGGTAGCCGT

Figure 5: Shc polynucleotide sequence alignments

Cloned ac 43030: Cloned *Alicyclobacillus acidocaldarius* ATCC43030
 Cloned at 43030: Cloned *Alicyclobacillus acidoterrestris* ATCC49025
 5 Blast ac: sequence of *A. acidocaldarius* got from the blast database
 Blast at: sequence of *A. acidocaldarius* got from the blast database

Primer and probe ranges were highlighted red

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10      G G G G G T T G G A T G T T C C A G G C Majority
      -----+-----
              10                      20
      -----+-----

15      1 G G G G G T T G G A T G T T A C A G G C cloned ac 43030 shc
      1 G G A G G A T G G A T G T T T C A G G C Blast ac shc
      1 G G A G G G T G G A T G T T C C A G G C cloned at 49025 shc
      1 G G G G G T T G G A T G T T C C A G G C Blast at shc

20      T T G T A T T T C T C C A G T G T G G G Majority
      -----+-----
              30                      40
      -----+-----

25      21 T T C C A T C T C G C C C G T G T G G G cloned ac 43030 shc
      21 T T C C A T C T C G C C G G T G T G G G Blast ac shc
      21 G A G T A T T T C T C C A A T C T G G G cloned at 49025 shc
      21 G A G T A T T T C T C C A A T C T G G G Blast at shc

30      A T A C T G G C T T G G C C G T G T T G Majority
      -----+-----
              50                      60
      -----+-----

35      41 A C A C G G G T C T C G C C G T G C T C cloned ac 43030 shc
      41 A C A C G G G C C T C G C C G T G C T C Blast ac shc
      41 A T A C T G G C T T G A C C G T C T T G cloned at 49025 shc
      41 A T A C T G G C T T G A C C G T C T T G Blast at shc

40      G C G C T G C G T T C T G C T G G G T T Majority
      -----+-----
              70                      80
      -----+-----

45      61 G C G C T G C G C G C T G C G G G G C T cloned ac 43030 shc
      61 G C G C T G C G C G C T G C G G G G C T Blast ac shc
      61 G C A C T G C G T T C G G C T G G A T T cloned at 49025 shc
      61 G C A C T G C G T T C G G C T G G A T T Blast at shc

50      T C C G G C C G A T C A T - G C C G G G Majority
      -----+-----
              90                      100
      -----+-----

55      81 T C C G G C C G A T C A C T G A C C G G cloned ac 43030 shc
      81 T C C G G C C G A T C A C - G A C C G C Blast ac shc
      81 G C C A C C A G A T C A T - C C A G C G cloned at 49025 shc
      81 G C C A C C A G A T C A T - C C A G C G Blast at shc
  
```

Figure 5: Shc polynucleotide sequence alignments (continued)

		T T G G T T A A G G C - - G G G T G A G	Majority
5		-----+-----+-	
		110 120	
		-----+-----+-	
	101	T T G G T C A A G G C T G G G C T G A A	cloned ac 43030 shc
	100	T T G G T C A A G G C - - G G G C G A G	Blast ac shc
10	100	C T G A T T A A A G C - - G G G T G A G	cloned at 49025 shc
	100	C T G A T T A A A G C - - G G G T G A G	Blast at shc
		T G G T T G T T G G G T C G G C A G A T	Majority
		-----+-----+-	
15		130 140	
		-----+-----+-	
	121	T G G C T G T T G G A C C G G C A G A T	cloned ac 43030 shc
	118	T G G C T G T T G G A C C G G C A G A T	Blast ac shc
	118	T G G T T G G T C A G T A A A C A A A T	cloned at 49025 shc
20	118	T G G T T G G T C A G T A A A C A A A T	Blast at shc
		T C T C G T G G C T G G C G A C T G G G	Majority
		-----+-----+-	
25		150 160	
		-----+-----+-	
	141	C A C C G T G C C G G G C G A T T G G G	cloned ac 43030 shc
	138	C A C G G T T C C G G G C G A C T G G G	Blast ac shc
	138	T C T C A A G G A T G G C G A C T G G A	cloned at 49025 shc
30	138	T C T C A A G G A T G G C G A C T G G A	Blast at shc
		A G G T T C G T C G C C G G A A G G T G	Majority
		-----+-----+-	
		170 180	
		-----+-----+-	
35	161	T G G T G A A G C G C C C G A A C C T C	cloned ac 43030 shc
	158	C G G T G A A G C G C C C G A A C C T C	Blast ac shc
	158	A A G T T C G T C G A C G C A A G G C G	cloned at 49025 shc
	158	A A G T T C G T C G A C G C A A G G C G	Blast at shc
40		A A A C C G G G C G G T T T G G C G T T	Majority
		-----+-----+-	
		190 200	
		-----+-----+-	
	181	A A C C C G G G C G G C T T C G C G C T	cloned ac 43030 shc
45	178	A A G C C G G G C G G G T T C G C G T T	Blast ac shc
	178	A A A C C A G G C G G T T G G G C A T T	cloned at 49025 shc
	178	A A A C C A G G C G G T T G G G C A T T	Blast at shc
		T G A G T T C G A C T G C G T G T A C T	Majority
		-----+-----+-	
50		210 220	
		-----+-----+-	
	201	C C A G T T C G A C A A C G T G T A C T	cloned ac 43030 shc
	198	C C A G T T C G A C A A C G T G T A C T	Blast ac shc
55	198	T G A A T T C C A C T G C G A A A A C T	cloned at 49025 shc
	198	T G A A T T C C A C T G C G A A A A C T	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		A C C C G G A C G T G G A C G A T A C G	Majority
		-----+-----	
5		230 240	
		-----+-----	
	221	A T C C G G A C G T G G A C G A C A C G	cloned ac 43030 shc
	218	A C C C G G A C G T G G A C G A C A C G	Blast ac shc
	218	A C C C A G A C G T C G A C G A T A C G	cloned at 49025 shc
10	218	A C C C A G A C G T C G A C G A T A C G	Blast at shc
		G C G G T G G T C G T C T T G G C G C T	Majority
		-----+-----	
		250 260	
		-----+-----	
15	241	G C C G T C G T C A T C T G G G C G C T	cloned ac 43030 shc
	238	G C C G T C G T G G T G G G C G C T	Blast ac shc
	238	G C G A T G G T C G T C T T G G C G C T	cloned at 49025 shc
	238	G C G A T G G T C G T C T T G G C G C T	Blast at shc
20		C A A T G G C C T T C G A T T G C C G G	Majority
		-----+-----	
		270 280	
		-----+-----	
25	261	C A A C A C G C T G C G A C T C C C G G	cloned ac 43030 shc
	258	C A A C A C C C T G C G C T T G C C G G	Blast ac shc
	258	C A A T G G C A T T C A A T T G C C G G	cloned at 49025 shc
	258	C A A T G G C A T T C A A T T G C C G G	Blast at shc
30		A T G A G G G G C G G C G T C G T G A C	Majority
		-----+-----	
		290 300	
		-----+-----	
35	281	A C G A G C G C C G C A G G C G A G A C	cloned ac 43030 shc
	278	A C G A G C G C C G C A G G C G G G A C	Blast ac shc
	278	A T G A A G G G A A G C G T C G T G A C	cloned at 49025 shc
	278	A T G A A G G G A A G C G T C G T G A C	Blast at shc
		G C C T T G A C G C G T G G C T T C C G	Majority
40		-----+-----	
		310 320	
		-----+-----	
	301	G C C A T G A C G A A G G G A T T C C G	cloned ac 43030 shc
	298	G C C A T G A C G A A G G G A T T C C G	Blast ac shc
45	298	G C A T T G A C C C G T G G C T T C C G	cloned at 49025 shc
	298	G C A T T G A C C C G T G G C T T C C G	Blast at shc
		T T G G T T T G T C G G G A T G C A G A	Majority
		-----+-----	
		330 340	
		-----+-----	
50			
	321	C T G G A T T G T C G G C <u>A T G C A G A</u>	cloned ac 43030 shc
	318	C T G G A T T G T C G G C <u>A T G C A G A</u>	Blast ac shc
	318	T T G G T T G C G C G A G <u>A T G C A G A</u>	cloned at 49025 shc
55	318	T T G G T T G C G C G A G <u>A T G C A G A</u>	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		G T T C G A A C G G G G C T G G G G C	Majority
		-----+-----+	
5		350 360	
		-----+-----+	
	341	G C T C G A A C G G C G G C T G G G G C	cloned ac 43030 shc
	338	G C T C G A A C G G C G G T T G G G G C	Blast ac shc
	338	G T T C G A A C G G G G G C T G G G G C	cloned at 49025 shc
10	338	G T T C G A A C G G G G G C T G G G G C	Blast at shc
		G C A T A C G A T G T G G A C A A C A C	Majority
		-----+-----+	
		370 380	
		-----+-----+	
15	361	G C A T A C G A C G T C G A C A A C A C	cloned ac 43030 shc
	358	G C C T A C G A C G T C G A C A A C A C	Blast ac shc
	358	G C A T A C G A T G T G G A C A A C A C	cloned at 49025 shc
	358	G C A T A C G A T G T G G A C A A C A C	Blast at shc
20			
		G C G T G A T T T G C C G A A - T C G G	Majority
		-----+-----+	
		390 400	
		-----+-----+	
25	381	G A G C G A T C T C C C G A A - C C A C	cloned ac 43030 shc
	378	G A G C G A T C T C C C G A A - C C A C	Blast ac shc
	378	G C G T C A G T T G A C C A A - T C G G	cloned at 49025 shc
	378	G C G T C A G T T G A C C A A A T C G G	Blast at shc
30			
		A T T C C G T T T T - G C G A C T T C G	Majority
		-----+-----+	
		410 420	
		-----+-----+	
35	400	A T C C C G T T C T - G C G A C T T C G	cloned ac 43030 shc
	397	A T C C C G T T C T - G C G A C T T C G	Blast ac shc
	397	A T T C C A T T T T - G C A A C T T C G	cloned at 49025 shc
	398	A T T C C A T T T T T G C G A C T T C G	Blast at shc
40			
		G - C G A A G T G A T T G A T C C G C C	Majority
		-----+-----+	
		430 440	
		-----+-----+	
45	419	G - C G A A G T G A C C G A T C C G C C	cloned ac 43030 shc
	416	G - C G A A G T G A C C G A T C C G C C	Blast ac shc
	416	G - C G A A G T G A T T G A T C C G C C	cloned at 49025 shc
	418	G G C G A A G T G A T T G A T C C G C C	Blast at shc
50			
		G T C G G A A G A C G T C A C C G C C C	Majority
		-----+-----+	
		450 460	
		-----+-----+	
	438	G T C G G A A G A C G T C A C C G C C C	cloned ac 43030 shc
	435	G T C A G A G G A C G T C A C C G C C C	Blast ac shc
	435	A T C G G A A G A C G T C A C C G C C A C	cloned at 49025 shc
55	438	A T C G G A A G A C G T C A C C G C C A C	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

	A C G T G T T G G A G T G T T T C G G C	Majority
	-----+-----	
5	470 480	
	-----+-----	
458	A C G T G C T C <u>G A G T G T T T C G G C</u>	cloned ac 43030 shc
455	A C G T G C T C <u>G A G T G T T T C G G C</u>	Blast ac shc
455	A C G T C T T G <u>G A G T G C T T C G G C</u>	cloned at 49025 shc
10 458	A C G T C T T G <u>G A G T G C T T C G G C</u>	Blast at shc
	A G C T T T G G G T A C G A C G A G G C	Majority
	-----+-----	
	490 500	
	-----+-----	
15 478	<u>A G C T T</u> C G G C T A C G A C G A C G C	cloned ac 43030 shc
475	<u>A G C T T</u> C G G G T A C G A T G A C G C	Blast ac shc
475	<u>A G C T T</u> T G G G T A C G A C G A G G C	cloned at 49025 shc
20 478	<u>A G C T T</u> T G G G T A C G A C G A G G C	Blast at shc
	C T G G A A G G T G A T T C G G C G G G	Majority
	-----+-----	
	510 520	
	-----+-----	
25 498	C T G G A A G G T G A T C C A G C G C G	cloned ac 43030 shc
495	C T G G A A G G T C A T C C G G C G C G	Blast ac shc
495	A T G G A A G G T G A T T C G C A A G G	cloned at 49025 shc
498	A T G G A A G G T G A T T C G C A A G G	Blast at shc
30	C G G T G G A G T A T C T C A A G G G G	Majority
	-----+-----	
	530 540	
	-----+-----	
35 518	C G G T G G C G T A C C T C A A G C G G	cloned ac 43030 shc
515	C G G T G G A A T A T C T C A A G C G G	Blast ac shc
515	C G G T C G A G T A T C T C A A G G C G	cloned at 49025 shc
518	C G G T C G A G T A T C T C A A G G C G	Blast at shc
	G A G C A G C G G C C G G A T G G G T G	Majority
	-----+-----	
	550 560	
	-----+-----	
45 538	G A G C A G A A G C C G G A C G G C A G	cloned ac 43030 shc
535	G A G C A G A A G C C G G A C G G C A G	Blast ac shc
535	C A A C A A C G C C C A G A T G G G T C	cloned at 49025 shc
538	C A A C A A C G C C C A G A T G G G T C	Blast at shc
	C T G G T T T G G T C G C T G G G G C G	Majority
	-----+-----	
	570 580	
	-----+-----	
50 558	C T G G T T C G G T C G C T G G G G C G	cloned ac 43030 shc
555	C T G G T T C G G T C G T T G G G G C G	Blast ac shc
555	A T G G T T T G G C C G C T G G G G C G	cloned at 49025 shc
55 558	A T G G T T T G G C C G C T G G G G C G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		T C A A C T A C G T G T A T G G C A T G	Majority
		-----+-----+-----	
5		590 600	
		-----+-----+-----	
	578	T C A A C T A C A T C T A C G G C A C G	cloned ac 43030 shc
	575	T C A A T T A C C T C T A C G G C A C G	Blast ac shc
10	575	T C A A C T A C G T G T A T G G C A T C	cloned at 49025 shc
	578	T C A A C T A C G T G T A T G G C A T C	Blast at shc
		G G C G C G G T G G T T T C G G G G C T	Majority
		-----+-----+-----	
		610 620	
		-----+-----+-----	
15	598	G G C G C G G T G G T G T C G G C G C T	cloned ac 43030 shc
	595	G G C G C G G T G G T G T C G G C G C T	Blast ac shc
	595	G G C G C G G T C G T T C C G G G A C T	cloned at 49025 shc
20	598	G G C G C G G T C G T T C C G G G A C T	Blast at shc
		G A A G G C G G T C G G T G T C G A T A	Majority
		-----+-----+-----	
		630 640	
		-----+-----+-----	
25	618	G A A G G C G G T C G G G A T C G A C A	cloned ac 43030 shc
	615	G A A G G C G G T C G G G A T C G A C A	Blast ac shc
	615	C A A G G C C G T C G G T G T C G A T A	cloned at 49025 shc
	618	C A A G G C C G T C G G T G T C G A T A	Blast at shc
30		T G C G T G A G C C G T G G G T T C A A	Majority
		-----+-----+-----	
		650 660	
		-----+-----+-----	
35	638	T G C G C G A G C C G T A C A T T C A A	cloned ac 43030 shc
	635	C G C G C G A G C C G T A C A T T C A A	Blast ac shc
	635	T G C G T G A G C C G T G G G T G C A A	cloned at 49025 shc
	638	T G C G T G A G C C G T G G G T G C A A	Blast at shc
		A A G T C G C T C G A C T G G G T C G T	Majority
		-----+-----+-----	
		670 680	
		-----+-----+-----	
40	658	A A G G C G C T C G A T T G G G T G G A	cloned ac 43030 shc
	655	A A G G C G C T C G A C T G G G T C G A	Blast ac shc
45	655	A A G T C G C T C G A C T G G C T C G T	cloned at 49025 shc
	658	A A G T C G C T C G A C T G G C T C G T	Blast at shc
		G G A G C A T C A G A A T G C G G A T G	Majority
		-----+-----+-----	
		690 700	
		-----+-----+-----	
50	678	G C A G C A T C A G A A C C C G G A C G	cloned ac 43030 shc
	675	G C A G C A T C A G A A C C C G G A C G	Blast ac shc
	675	C G A G C A T C A A A A T G A G G A T G	cloned at 49025 shc
55	678	C G A G C A T C A A A A T G A G G A T G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		G C G G C T G G G G T G A A G A C T G - Majority	
		-----+-----	
5		710 720	
		-----+-----	
	698	G	cloned ac 43030 shc
	695	G C G G C T G G G G C G A G G A C T G -	Blast ac shc
	695	G C G G C T G G G G T G A A A G C C G A	cloned at 49025 shc
10	698	G C G G T T G G G G T G A A G A T T G -	Blast at shc
		- - C C G X T C X T A C G A G G A T C C Majority	
		-----+-----	
		730 740	
		-----+-----	
15	698		cloned ac 43030 shc
	714	- - C C G C T C G T A C G A G G A T C C	Blast ac shc
	715	A T T C C A G C A C A C T G G C G G C C	cloned at 49025 shc
	717	- - C C G T T C C T A T G A T G A T C C	Blast at shc
20		G X X X C T C G C G G G T C A G G G C G Majority	
		-----+-----	
		750 760	
		-----+-----	
25	698		cloned ac 43030 shc
	732	G G C G T A C G C G G G T A A G G G C G	Blast ac shc
	735	G T T A C T A G T G G A T C C G A G C T	cloned at 49025 shc
	735	A C G T C T C G C A G G T C A G G G T G	Blast at shc
30		C G A G X A C A C C G T C G C A G A C X Majority	
		-----+-----	
		770 780	
		-----+-----	
35	698		cloned ac 43030 shc
	752	C G A G C <u>A C C C C G T C G C A G A C G</u>	Blast ac shc
	755	C G G T A <u>C C A A G C T T G G C G T A A</u>	cloned at 49025 shc
	755	T G A G T <u>A C A C C G T C G C A G A C C</u>	Blast at shc
40		G C C T G G G C G T T G A T G G C G C T Majority	
		-----+-----	
		790 800	
		-----+-----	
45	698		cloned ac 43030 shc
	772	<u>G C C T G G G C G C T G A T G G C G C T</u>	Blast ac shc
	775	<u>T C A T G G T C A T A G C T G T T T C C</u>	cloned at 49025 shc
	775	<u>G C C T G G G C G G T T G A T G G C G C T</u>	Blast at shc
50		C A T C G C G G G C G G C X G T G T C G Majority	
		-----+-----	
		810 820	
		-----+-----	
	698		cloned ac 43030 shc
	792	<u>C A T C G C G G G C G G C</u> A G G G C G G	Blast ac shc
	795	<u>T G T G T G A A A T T G - -</u> G T A T C C	cloned at 49025 shc
55	795	C A T C G C G G G C G G C C G T G T C G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		A G T C A G A X G C C G C A C X X C G C	Majority
		-----+-----+--	
5		830 840	
		-----+-----+--	
	698		cloned ac 43030 shc
	812	A G T C C G A G G C C G C G C G C C G C	Blast ac shc
	813	G C T C A C A A T T C A C A C A A C A T	cloned at 49025 shc
10	815	A G T C A G A T G C G G T A T T G C G C	Blast at shc
		G G G G T C C X X T A C C T X X X X G -	Majority
		-----+-----+--	
		850 860	
		-----+-----+--	
15	698		cloned ac 43030 shc
	832	G G C G T G C A A T A C C T C G T G G -	Blast ac shc
	833	A C G A G C C G G A A C A T A A G T G T	cloned at 49025 shc
	835	G G G G T C A C T T A C C T T C A C G -	Blast at shc
20		A X A C G C A G C G C G C X G A T G - G	Majority
		-----+-----+--	
		870 880	
		-----+-----+--	
25	698		cloned ac 43030 shc
	851	A G A C G C A G C G C C C G G A C G - G	Blast ac shc
	853	A A G C C T G G G G T G C C T A T G A G	cloned at 49025 shc
	854	A C A C G C A G C G C G C A G A T G - G	Blast at shc
30		T G G C T G X X X	Majority

35	698		cloned ac 43030 shc
	870	C G G C T G G G A	Blast ac shc
	873	T G A G C T	cloned at 49025 shc
	873	T G G C T G	Blast at shc

Figure 6: Shc amino acid sequence alignments

The degenerate primer range is highlighted red.

5	M T - - - - - E Q L V E A - Majority	
	-----+-----+--	
	10 20	
	-----+-----+--	
10	1 M A - - - - - E Q L V E A - A. acidocaldarius ATCC27009	
	1 M A - - - - - E Q L V E A - A. acidocaldarius JCM 5260T	
	1 M T - - - - - K Q L L D T - A. acidoterrestris DSM 3902	
	1 M G T - - - - - Bacillus subtilis	
	1 F T R M T T T N W S L K V D R G R Q T W Dictyostelium discoideum	
	1 M V I A A S - - - - - Synechocystis sp. PCC 6803	
15	1 M T A T T D G S T G A S L R P L A A S - Streptomyces coelicolor A3	
	- - - - - P - - - - - Majority	
	-----+-----+--	
	30 40	
	-----+-----+--	
20	9 - - - - - P - - - - - A. acidocaldarius ATCC27009	
	9 - - - - - P - - - - - A. acidocaldarius JCM 5260T	
	9 - - - - - P - - - - - A. acidoterrestris DSM 3902	
	4 - - - - - Bacillus subtilis	
25	21 E Y S Q E K K E A T D V D I H L L R L K Dictyostelium discoideum	
	7 - - - - - Synechocystis sp. PCC 6803	
	20 - - - - - A S D T D I T I - - - - Streptomyces coelicolor A3	
	- - - - - E A V A R Majority	
30	-----+-----+--	
	50 60	
	-----+-----+--	
35	10 - - - - - A Y A R A. acidocaldarius ATCC27009	
	10 - - - - - A Y A R A. acidocaldarius JCM 5260T	
	10 - - - - - M V Q A A. acidoterrestris DSM 3902	
	4 - - - - - L - - - - - Q E K V R R Bacillus subtilis	
	41 E P G T H C P E G C D L N R A K T P Q Q Dictyostelium discoideum	
	7 - P S V P C P S - - - - - T E Q V R Q Synechocystis sp. PCC 6803	
	28 - P A A A A G V - - - - - P E A A A R Streptomyces coelicolor A3	
40	A L D R A V D Y L L S R Q K A D G Y W W Majority	
	-----+-----+--	
	70 80	
	-----+-----+--	
45	14 T L D R A V E Y L L S C Q K D E G Y W W A. acidocaldarius ATCC27009	
	14 T L D R A V E Y L L S C Q K D E G Y W W A. acidocaldarius JCM 5260T	
	14 T L E A G V A H L L R R Q A P D G Y W W A. acidoterrestris DSM 3902	
	11 F Q K K T I T E L R D R Q N A D G S W T Bacillus subtilis	
	61 A I K K A F Q Y F S K V Q T E D G H W A Dictyostelium discoideum	
50	20 A I A A S R D F L L S E Q Y A D G Y W W Synechocystis sp. PCC 6803	
	41 A T R R A T D F L L A K Q D A E G W W K Streptomyces coelicolor A3	

Figure 6: Shc amino acid sequence alignments (continued)

		G P L L S N V T M E A E Y V L L C H I L	Majority
		-----+-----+-----	
5		90 100	
		-----+-----+-----	
	34	G P L L S N V T M E A E Y V L L C H I L	A. acidocaldarius ATCC27009
	34	G P L L S N V T M E A E Y V L L C H I L	A. acidocaldarius JCM 5260T
	34	A P L L S N V C M E A E Y V L L C H C L	A.acidoterrestris DSM 3902
10	31	F C F E G P I M T N S F F I L L L T S L	Bacillus subtilis
	81	G D Y G G P M F L L P G L V I T C Y V T	Dictyostelium discoideum
	40	S E L E S N V T I T A E V V I L H K I W	Synechocystis sp. PCC 6803
	61	G D L E T N V T M D A E D L L L R Q F L	Streptomyces coelicolor A3
15		G R V D R E R - - M E K I R R Y L L H E	Majority
		-----+-----+-----	
		110 120	
		-----+-----+-----	
	54	D R V D R D R - - M E K I R R Y L L H E	A. acidocaldarius ATCC27009
20	54	D R V D R D R - - M E K I R R Y L L H E	A. acidocaldarius JCM 5260T
	54	G K K N P E R - - E A Q I R K Y I I S Q	A.acidoterrestris DSM 3902
	51	D E G E N E K E L I S S L A A G I H A K	Bacillus subtilis
	101	G Y Q L P E S T Q R E I I R Y L F N R Q	Dictyostelium discoideum
	60	G T A A Q R P - - L E K A K N Y L L Q Q	Synechocystis sp. PCC 6803
25	81	G I Q D E E T - - T R A A A L F I R G E	Streptomyces coelicolor A3
		Q R E D G T W A L Y P G G P - G D L S T	Majority
		-----+-----+-----	
		130 140	
		-----+-----+-----	
30	72	Q R E D G T W A L Y P G G P - P D L D T	A. acidocaldarius ATCC27009
	72	Q R E D G T W A L Y P G G P - P D L D T	A. acidocaldarius JCM 5260T
	72	R R E D G T W S I Y P G G P - S D L N A	A.acidoterrestris DSM 3902
	71	Q Q P D G T F I N Y P D E T R G N L T A	Bacillus subtilis
35	121	N P V D G G W G L H I E A H S D I F G T	Dictyostelium discoideum
	78	Q R D H G G W E L Y Y G D G - G E L S T	Synechocystis sp. PCC 6803
	99	Q R E D G T W A T F Y G G P - G E L S T	Streptomyces coelicolor A3
40		T V E A Y V A L K Y L G - V S A D E P H	Majority
		-----+-----+-----	
		150 160	
		-----+-----+-----	
	91	T I E A Y V A L K Y I G - M S R D E E P	A. acidocaldarius ATCC27009
	91	T I E A Y V A L K Y I G - M S R D E E P	A. acidocaldarius JCM 5260T
45	91	T V E A Y V A L K Y L G - E P A S D P Q	A.acidoterrestris DSM 3902
	91	T V Q G Y V G M L A S G C F H R T E P H	Bacillus subtilis
	141	T L Q - Y V S L R L L G - V P A D H P S	Dictyostelium discoideum
	97	S V E A Y T A L R I L G - V P A T D P A	Synechocystis sp. PCC 6803
	118	T I E A Y V A L R L A G - D S P E A P H	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		M V K A L E F I Q S Q G G I E S S R V F	Majority
		-----+-----+-----	
5		170 180	
		-----+-----+-----	
	110	M Q K A L R F I Q S Q G G I E S S R V F	A. acidocaldarius ATCC27009
	110	M Q K A L R F I Q S Q G G I E S S R V F	A. acidocaldarius JCM 5260T
	110	M V Q A K E F I Q N E G G I E S T R V F	A.acidoterrestris DSM 3902
10	111	M K K A E Q F I I S H G G L R H V H F M	Bacillus subtilis
	159	V V K A R T F L L Q N G G A T G I P S W	Dictyostelium discoideum
	116	L V K A K N F I V G R G G I S K S R I F	Synechocystis sp. PCC 6803
	137	M A R A A E W I R S R G G I A S A R V F	Streptomyces coelicolor A3
15		T R M W L A L V G E Y P W D K L P M I P	Majority
		-----+-----+-----	
		190 200	
		-----+-----+-----	
	130	T R M W L A L V G E Y P W E K V P M V P	A. acidocaldarius ATCC27009
20	130	T R M W L A L V G E Y P W E K V P M V P	A. acidocaldarius JCM 5260T
	130	T R L W L A M V G Q Y P W D K L P V I P	A.acidoterrestris DSM 3902
	131	T K W M L A A N G L Y P W P A L - Y L P	Bacillus subtilis
	179	G K F W L A T L N A Y D W N G L N P I P	Dictyostelium discoideum
	136	T K M H L A L I G C Y D W R G T P S I P	Synechocystis sp. PCC 6803
25	157	T R I W L A L F G W W K W D D L P E L P	Streptomyces coelicolor A3
		P E I M L L P K N V P L N I Y E F G S W	Majority
		-----+-----+-----	
		210 220	
		-----+-----+-----	
30	150	P E I M F L G K R M P L N I Y E F G S W	A. acidocaldarius ATCC27009
	150	P E I M F L G K R M P L N I Y E F G S W	A. acidocaldarius JCM 5260T
	150	P E I M H L P K S V P L N I Y D F A S W	A.acidoterrestris DSM 3902
	150	L S L M A L P P T L P I H F Y Q F S S Y	Bacillus subtilis
35	199	I E F W L L P Y N L P I A P G R W W C H	Dictyostelium discoideum
	156	P W V M L L P N N F F F N I Y E M S S W	Synechocystis sp. PCC 6803
	177	P E L I Y F P T W V P L N I Y D F G C W	Streptomyces coelicolor A3
40		A R A T V V P L S I V M A Q Q P V - - -	Majority
		-----+-----+-----	
		230 240	
		-----+-----+-----	
	170	A R A T V V A L S I V M S R Q P V - - -	A. acidocaldarius ATCC27009
	170	A R A T V V A L S I V M S R Q P V - - -	A. acidocaldarius JCM 5260T
45	170	A R A T I V T L S Y R H E S P T C - - -	A.acidoterrestris DSM 3902
	170	A R I H F A P M A V T L N Q R - - - -	Bacillus subtilis
	219	C R M V Y L P M S Y I Y A K K T T G P L	Dictyostelium discoideum
	176	A R S S T V P L M I V C D Q K P V - - -	Synechocystis sp. PCC 6803
	197	A R Q T I V P L T I V S A K R P V R P A	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		- F P L P E L A R V P E L Y E T D V P P	Majority
		-----+-----+-----	
5		250 260	
		-----+-----+-----	
	187	- F P L P E R A R V P E L Y E T D V P P	A. acidocaldarius ATCC27009
	187	- F P L P E R A R V P E L Y E T D V P P	A. acidocaldarius JCM 5260T
	187	- D A T S G L C K G S G I V R G E G P P	A.acidoterrestris DSM 3902
10	185	- F V L I N R - N I S S L H H L D - - P	Bacillus subtilis
	239	T D L V K D L R R - - E I Y C Q E Y E K	Dictyostelium discoideum
	193	- Y D I A Q G L R V D E L Y A E G M E N	Synechocystis sp. PCC 6803
	217	P F P L D E L H T D P A - - - R P N P P	Streptomyces coelicolor A3
15		R R - R G A K G G G G W - - - I F D A -	Majority
		-----+-----+-----	
		270 280	
		-----+-----+-----	
	206	R R - R G A K G G G G W - - - I F D A -	A. acidocaldarius ATCC27009
20	206	R R - R G A K G G G G W - - - I F D A -	A. acidocaldarius JCM 5260T
	206	K R - R S A K G G D S G - - - F F V A -	A.acidoterrestris DSM 3902
	201	H M T K N P F T W L R S - - D A F E E R	Bacillus subtilis
	257	I N W S E Q R N N I S K L D M Y Y E H T	Dictyostelium discoideum
	212	V Q Y K L P E S G T I W - - D I F I G -	Synechocystis sp. PCC 6803
25	234	R P - L A P V A S W D G - - - A F Q R -	Streptomyces coelicolor A3
		- L D S A L H G Y Q K A - - A V H P F R	Majority
		-----+-----+-----	
		290 300	
		-----+-----+-----	
30	221	- L D R A L H G Y Q K L - - S V H P F R	A. acidocaldarius ATCC27009
	221	- L D R A L H G Y Q K L - - S V H P F R	A. acidocaldarius JCM 5260T
	221	- L D K F L K A Y N K W - - P I Q P G R	A.acidoterrestris DSM 3902
	219	D L T S I L L H W K R V F H A P F A F Q	Bacillus subtilis
35	277	S L L N V I N G S L N A Y E K V H S K W	Dictyostelium discoideum
	229	- L D S L F K L Q E Q A - - K V V P F R	Synechocystis sp. PCC 6803
	249	- I D K A L H A Y R K V - - A P R R L R	Streptomyces coelicolor A3
40		R A G E A R A L T W I L E R Q E G D G S	Majority
		-----+-----+-----	
		310 320	
		-----+-----+-----	
	238	R A A E I R A L D W L L E R Q A G D G S	A. acidocaldarius ATCC27009
	238	R A A E I R A L D W L L E R Q A G D G S	A. acidocaldarius JCM 5260T
45	238	K S G E Q K A L E W I L A H Q E A D G C	A.acidoterrestris DSM 3902
	239	Q L G L Q T A K T Y M L D R I E K D G T	Bacillus subtilis
	297	L R D K A I D Y T F D H I R Y E D E Q T	Dictyostelium discoideum
	246	E Q G L A L A E K W I L E R Q E V S G D	Synechocystis sp. PCC 6803
	266	R A A M N S A A R W I I E R Q E N D G C	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		W G G I Q P P W F Y A L I A L K V L G M	Majority
		-----+-----+-----	
5		330 340	
		-----+-----+-----	
	258	W G G I Q P P W F Y A L I A L K I L D M	A. acidocaldarius ATCC27009
	258	W G G I Q P P W F Y A L I A L K I L D M	A. acidocaldarius JCM 5260T
	258	W G G I Q P P W F Y A L L A L K C L N M	A. acidoterrestris DSM 3902
10	259	L Y S Y A S A T I Y M V Y S L L S L G V	Bacillus subtilis
	317	K Y I D I G P V N K T V N M L C V W D R	Dictyostelium discoideum
	266	W G G I I P A M L N S L L A L K V L G Y	Synechocystis sp. PCC 6803
	286	W G G I Q P P A V Y S V I A L Y L L G Y	Streptomyces coelicolor A3
15		T - Q H P A F I K G L E G L E L Y G V E	Majority
		-----+-----+-----	
		350 360	
		-----+-----+-----	
	278	T - Q H P A F I K G W E G L E L Y G V E	A. acidocaldarius ATCC27009
20	278	T - Q H P A F I K G W E G L E L Y G V E	A. acidocaldarius JCM 5260T
	278	T - D H P A F V K G F E G L E A Y G V H	A. acidoterrestris DSM 3902
	279	S R Y S P I I R R A I T G I K S L V T K	Bacillus subtilis
	337	E G K S P A F Y K H A D R L K D Y - L W	Dictyostelium discoideum
	286	D V N D L Y V Q R G L A A I D N F A V E	Synechocystis sp. PCC 6803
25	306	D L E H P V M R A G L E S L D R F A V W	Streptomyces coelicolor A3
		L S D G G W M F Q A - S I S P V W D T G	Majority
		-----+-----+-----	
		370 380	
		-----+-----+-----	
30	297	L D Y G G W M F Q A - S I S P V W D T G	A. acidocaldarius ATCC27009
	297	L D Y G G W M F Q A - S I S P V W D T G	A. acidocaldarius JCM 5260T
	297	T S D G G W M F Q A - S I S P I W D T G	A. acidoterrestris DSM 3902
	299	C N G I P Y L - E N - S T S T V W D T A	Bacillus subtilis
35	356	L S F D G M K M Q G Y N G S Q L W D T A	Dictyostelium discoideum
	306	T E - D S Y A I Q A - C V S P V W D T A	Synechocystis sp. PCC 6803
	326	R E D G A R M I E A - C Q S P V W D T C	Streptomyces coelicolor A3
		L A V L A L R A A G L P A D H P A L V K	Majority
		-----+-----+-----	
40		390 400	
		-----+-----+-----	
	316	L A V L A L R A A G L P A D H D R L V K	A. acidocaldarius ATCC27009
	316	L A V L A L R A A G L P A D H D R L V K	A. acidocaldarius JCM 5260T
45	316	L T V L A L R S A G L P P D H P A L I K	A. acidoterrestris DSM 3902
	317	L I S Y A L Q K N G V T E T D G S V T K	Bacillus subtilis
	376	F T I Q A F M E S G I A N Q F Q D C M K	Dictyostelium discoideum
	324	W V V R A L A E A D L G K D H P A L V K	Synechocystis sp. PCC 6803
50	345	L A T I A L A D A G V P E D H P Q L V K	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		A G E W L L D R Q I T V P G D W A V K R	Majority
		-----+-----	
5		410 420	
		-----+-----	
	336	A G E W L L D R Q I T V P G D W A V K R	A. acidocaldarius ATCC27009
	336	A G E W L L D R Q I T V P G D W A V K R	A. acidocaldarius JCM 5260T
	336	A G E W L V S K Q I L K D G D W K V R R	A.acidoterrestris DSM 3902
10	337	A A D F L L E R Q H T K I A D W S V K N	Bacillus subtilis
	396	L A G H Y L D I S Q V P E D A R D M K H	Dictyostelium discoideum
	344	A G Q W L L D K Q I L T Y G D W Q I K N	Synechocystis sp. PCC 6803
	365	A S D W M L G E Q I V R P G D W S V K R	Streptomyces coelicolor A3
15		- - P N L K P G G W A F E F D N V N Y P	Majority
		-----+-----	
		430 440	
		-----+-----	
	356	- - P N L K P G G F A F Q F D N V Y Y P	A. acidocaldarius ATCC27009
20	356	- - P N L K P G G F A F Q F D N V Y Y P	A. acidocaldarius JCM 5260T
	356	- - R K A K P G G W A F E F H C E N Y P	A.acidoterrestris DSM 3902
	357	- - P N S V P G G W G F S N I N T N N P	Bacillus subtilis
	416	Y H R H Y S K G A W P F S T V D H G W P	Dictyostelium discoideum
	364	- - P H G E P G A W A F E F D N N F Y P	Synechocystis sp. PCC 6803
25	385	- - P G L P P G G W A F E F H N D N Y P	Streptomyces coelicolor A3
		D V D D T A V V V - - - L A L N G L R L	Majority
		-----+-----	
		450 460	
		-----+-----	
30	374	D V D D T A V V V - - - W A L N T L R L	A. acidocaldarius ATCC27009
	374	D V D D T A V V V - - - W A L N T L R L	A. acidocaldarius JCM 5260T
	374	D V D D T A M V V - - - L A L N G I Q L	A.acidoterrestris DSM 3902
	375	D C D D T T A V L - - - K A I P R N H S	Bacillus subtilis
35	436	I S D C T A E G I K S A L A L R S L P F	Dictyostelium discoideum
	382	D I D D T C V V M - - - M A L Q G I T L	Synechocystis sp. PCC 6803
	403	D I D D T A E V V - - - L A L R R V R H	Streptomyces coelicolor A3
		P D E E R R R D A I T K G F R W L L G M	Majority
		-----+-----	
		470 480	
		-----+-----	
40	391	P D E R R R R D A M T K G F R W I V G M	A. acidocaldarius ATCC27009
	391	P D E R R R R D A M T K G F R W I V G M	A. acidocaldarius JCM 5260T
45	391	P D E G K R R D A L T R G F R W L R E M	A.acidoterrestris DSM 3902
	392	P A A W - - - - - E R G V S W L L S M	Bacillus subtilis
	456	I E P I S L D R - I A D G I N V L L T L	Dictyostelium discoideum
	399	P D E E R K Q G A I N K A L Q W I A T M	Synechocystis sp. PCC 6803
	420	H D P E R V E K A I G R G V R W N L G M	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		Q S S N G G W G A Y D V D N T S D L P N	Majority
		-----+-----+-----	
5		490 500	
		-----+-----+-----	
	411	Q S S N G G W G A Y D V D N T S D L P N	A. acidocaldarius ATCC27009
	411	Q S S N G G W G A Y D V D N T S D L P N	A. acidocaldarius JCM 5260T
	411	Q S S N G G W G A Y D V D N T R Q L T K	A.acidoterrestris DSM 3902
10	406	Q N N D G G F S A F E K N V N H P L I R	Bacillus subtilis
	475	Q N G D G G W A S Y E N T R G P K W L E	Dictyostelium discoideum
	419	Q C K T G G W A A F D I D N D Q D W L N	Synechocystis sp. PCC 6803
	440	Q S K N G A W G A F D V D N T S A F P N	Streptomyces coelicolor A3
		H L P - F C D F G E V - I D P P S A D V	Majority
15		-----+-----+-----	
		510 520	
		-----+-----+-----	
	431	H I P - F C D F G E V - T D P P S E D V	A. acidocaldarius ATCC27009
	431	H I P - F C D F G E V - T D P P S E D V	A. acidocaldarius JCM 5260T
20	431	S D S I F A T S G E V - I D P P S E D V	A.acidoterrestris DSM 3902
	426	L L P L E S A E D A A - V D P S T A D L	Bacillus subtilis
	495	K F N P S E V F Q N I M I D Y S Y V E C	Dictyostelium discoideum
	439	Q L P - Y G D L K A M - I D P S T A D I	Synechocystis sp. PCC 6803
	460	R L P - F C D F G E V - I D P P S A D V	Streptomyces coelicolor A3
25		T A H V L E C L G S - - - F G - - - -	Majority
		-----+-----+-----	
		530 540	
		-----+-----+-----	
30	449	T A H V L E C F G S - - - F G - - - -	A. acidocaldarius ATCC27009
	449	T A H V L E C F G S - - - F G - - - -	A. acidocaldarius JCM 5260T
	450	T A H V L E C F G S - - - F G - - - -	A.acidoterrestris DSM 3902
	445	T G R V L H F L G E - - K V G - - - -	Bacillus subtilis
	515	S A A C I Q A M S A F R K H A P N H P R	Dictyostelium discoideum
35	457	T A R V V E M L G A - - - C G - - - -	Synechocystis sp. PCC 6803
	478	T A H V V E M L A V - - - E G - - - -	Streptomyces coelicolor A3
		Y D E A W K V I R R A V E Y L K R E Q E	Majority
		-----+-----+-----	
40		550 560	
		-----+-----+-----	
	461	Y D D A W K V I R R A V E Y L K R E Q K	A. acidocaldarius ATCC27009
	461	Y D D A W K V I R R A V E Y L K R E Q K	A. acidocaldarius JCM 5260T
	462	Y D E A W K V I R K A V E Y L K A Q Q R	A.acidoterrestris DSM 3902
45	458	F T E K H Q H I Q R A V K W L F E H Q E	Bacillus subtilis
	535	I K E I N R S I A R G V K F I K S I Q R	Dictyostelium discoideum
	469	L T M D S P R V E R G L T Y L L Q E Q E	Synechocystis sp. PCC 6803
	490	L A H D P R T - R R G I Q W L L D A Q E	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		Q D G S W F G R W G V N Y L Y G T G A V	Majority
		-----+-----	
5		570 580	
		-----+-----	
	481	P D G S W F G R W G V N Y L Y G T G A V	A. acidocaldarius ATCC27009
	481	P D G S W F G R W G V N Y L Y G T G A V	A. acidocaldarius JCM 5260T
	482	P D G S W F G R W G V N Y V Y G I G A V	A.acidoterrestris DSM 3902
10	478	Q N G S W Y G R W G V C Y I Y G T W A A	Bacillus subtilis
	555	Q D G S W L G S W G I C F T Y G T W F G	Dictyostelium discoideum
	489	Q D G S W F G R W G V N Y L Y G T S G A	Synechocystis sp. PCC 6803
	509	T D G S W F G R W G V N Y V Y G T G S V	Streptomyces coelicolor A3
15		V S A L K A V G L D T R E P Y I Q K A L	Majority
		-----+-----	
		590 600	
		-----+-----	
	501	V S A L K A V G I D T R E P Y I Q K A L	A. acidocaldarius ATCC27009
20	501	V S A L K A V G I D T R E P Y I Q K A L	A. acidocaldarius JCM 5260T
	502	V P G L K A V G V D M R E P W V Q K S L	A.acidoterrestris DSM 3902
	498	L T G M H A C G L T E S I P V Y K R L C	Bacillus subtilis
	575	I E G L V A S G E P L T S P S I V K A C	Dictyostelium discoideum
	509	L S A L A I Y D A Q R F A P Q I K T A I	Synechocystis sp. PCC 6803
25	529	I P A L T A A G L P T S H P A I R R A V	Streptomyces coelicolor A3
		D W L E S H Q N A D G G W G E D C R S Y	Majority
		-----+-----	
		610 620	
		-----+-----	
30	521	D W V E Q H Q N P D G G W G E D C R S Y	A. acidocaldarius ATCC27009
	521	D W V E Q H Q N P D G G W G E D C R S Y	A. acidocaldarius JCM 5260T
	522	D W L V E H Q N E D G G W G E D C R S Y	A.acidoterrestris DSM 3902
	518	V - - - - - - - - - - G S N P Y	Bacillus subtilis
35	595	K F L A S K Q R A D G G W G E S F K S -	Dictyostelium discoideum
	529	A W L L S C Q N A D G G W G E T C E S Y	Synechocystis sp. PCC 6803
	549	R W L E S V Q N E D G G W G E D L R S Y	Streptomyces coelicolor A3
40		E - D P E Y A G Q G A S T A S Q T A W A	Majority
		-----+-----	
		630 640	
		-----+-----	
	541	E - D P A Y A G K G A S T P S Q T A W A	A. acidocaldarius ATCC27009
	541	E - D P A Y A G K G A S T P S Q T A W A	A. acidocaldarius JCM 5260T
45	542	D - D P R L A G Q G V S T P S Q T A W A	A.acidoterrestris DSM 3902
	524	K M M T E - A G E N P A K A P K S K - -	Bacillus subtilis
	614	N V T K E Y V Q H E T S Q V V N T G W A	Dictyostelium discoideum
	549	K - N K Q L K G Q G N S T A S Q T A W A	Synechocystis sp. PCC 6803
	569	R Y V R E W S G R G A S T A S Q T G W A	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		L M A L I A G - - - - - G R A E - -	Majority
5		-----+-----+-----	
		650 660	
		-----+-----+-----	
	560	L M A L I A G - - - - - G R A E - -	A. acidocaldarius ATCC27009
	560	L M A L I A G - - - - - G R A E - -	A. acidocaldarius JCM 5260T
10	561	L M A L I A G - - - - - G R V E - -	A.acidoterrestris DSM 3902
	541	- - - - - - - - - - - - - - - -	Bacillus subtilis
	634	L L S L M S A - K Y P D R - - - - -	Dictyostelium discoideum
	568	L I G L L D A L K Y L P S L G Q D A K L	Synechocystis sp. PCC 6803
	589	L M A L L A A - - - - - G E R D - -	Streptomyces coelicolor A3
15		S E A A E R G V A Y L V E T Q R P D G G	Majority
		-----+-----+-----	
		670 680	
		-----+-----+-----	
20	571	S E A A R R G V Q Y L V E T Q R P D G G	A. acidocaldarius ATCC27009
	571	S E A A R R G V Q Y L V E T Q R P D G G	A. acidocaldarius JCM 5260T
	572	S D A V L R G V T Y L H D T Q R A D G G	A.acidoterrestris DSM 3902
	541	- - - - - - - - - - - - - - - -	Bacillus subtilis
	646	- E C I E R G I K F L I Q R Q Y P N G D	Dictyostelium discoideum
	588	T T A I E G G V A F L V Q G Q T P K G T	Synechocystis sp. PCC 6803
25	600	S K A V E R G V A W L A A T Q R E D G S	Streptomyces coelicolor A3
		W D E P Y Y T G T G F P G D F Y L G Y T	Majority
		-----+-----+-----	
		690 700	
		-----+-----+-----	
30	591	W D E P Y Y T G T A S P G D F Y L G Y T	A. acidocaldarius ATCC27009
	591	W D E P Y Y T G T G F P G D F Y L G Y T	A. acidocaldarius JCM 5260T
	592	W D E E V Y T G T G F P G D F Y L A Y T	A.acidoterrestris DSM 3902
	541	- - - - - - - - - - - - - - - H	Bacillus subtilis
35	665	F P Q E S I I G V - F N F N C M I S Y S	Dictyostelium discoideum
	608	W E E A E Y T G T G F P C H F Y I R Y H	Synechocystis sp. PCC 6803
	620	W D E P Y F T G T G F P W D F S I N Y N	Streptomyces coelicolor A3
40		M Y R Q V F P L L A L G R Y K Q A - - -	Majority
		-----+-----+-----	
		710 720	
		-----+-----+-----	
45	611	M Y R H V F P T L A L G R Y K Q A - - -	A. acidocaldarius ATCC27009
	611	M Y R H V F P T L A L G R Y K Q A - - -	A. acidocaldarius JCM 5260T
	612	M Y R D I L P V W A L G R Y Q E A - - -	A.acidoterrestris DSM 3902
	542	M Y R F I - - - - - - - - - E E P L	Bacillus subtilis
	684	N Y K N I F P L W A L S R Y N Q - - - L	Dictyostelium discoideum
	628	Y Y R Q Y F P L I A L A R Y S H L Q A -	Synechocystis sp. PCC 6803
	640	L Y R Q V F P L T A L G R Y V H G E P F	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

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Figure 7

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1                               50
Z.bali sequencing (1) -----TGCATGGCCGTTCTTAGTTGGT
sacc. humal (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
cand. coll (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
grape (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
zygo. ruxil (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
PD sequencing (1) ----GTGCTGGAA--TTCCGCT---TTGCATGGCCGTTCTTAGTTGGT
BF sequencing (1) ----TGCTGGAA--TTCCGCT---TTGCATGGCCGTTCTTAGTTGGT
pen. cry (1) ---TCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
a. nidu (1) AGCTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
euro. amst (1) ----TTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
asp. cand (1) --CTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
chicken (1) --CTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
wheat (1) --CTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
Consensus (1) CTCTTTCTTGAT TT TGG TGGTGGTGCATGGCCGTTCTTAGTTGGT

51                               100
Z.bali sequencing (23) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTTAACCTACT
sacc. humal (49) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTTAACCTACT
cand. coll (49) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTTAACCTACT
grape (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTCAGCCTGCT
zygo. ruxil (49) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTTAACCTACT
PD sequencing (40) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTCGGCCCT-T
BF sequencing (39) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTCGGCCCT-T
pen. cry (48) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTCGGCCCT-T
a. nidu (51) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTCGGCCCT-T
euro. amst (46) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTCGGCCCT-T
asp. cand (49) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTCGGCCCT-T
chicken (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTCAGCCTGCT
wheat (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTCAGCCTGCT
Consensus (51) GGAGTGATTTGTCTGCTTAATTGCCATAACGAACGAGACCTCGGCCCT CT

101                               150
Z.bali sequencing (73) AAATAGT--GGTGCTA-GCATTTGCTGGTTTTTCCACTTCTTAGAGGGAC
sacc. humal (99) AAATAGT--GGTGCTA-GCATTTGCTGGTTAT-CCACTTCTTAGAGGGAC
cand. coll (99) AAATAGT--GGTGCTA-GCATTTGCTGGTTAT-CCACTTCTTAGAGGGAC
grape (99) AACTAGCTATGTGAAG-GTGAGCCTCCGCAGC-CAGCTTCTTAGAGGGAC
zygo. ruxil (99) AAATAGT--GGTGCTA-GCATTTGCTGGTTTTTCCACTTCTTAGAGGGAC
PD sequencing (89) AAATAGCCCGGTCC--GCATTTGCGGGGCGGC-TGGCTTCTTAGGGGGAC
BF sequencing (88) AAATAGCCCGGTCC--GCATTTGCGGGGCGGC-TGGCTTCTTAGGGGGAC
pen. cry (97) AAATAGCCCGGTCC--GCATTTGCGGGGCGGC-TGGCTTCTTAGGGGGAC
a. nidu (100) AAATAGCCCGGTCC--GCATTTGCGGGGCGGC-TGGCTTCTTAGGGGGAC
euro. amst (95) AAATAGCCCGGTCC--GCATTTGCGGGGCGGC-TGGCTTCTTAGGGGGAC
asp. cand (98) AAATAGCCCGGTCC--GCATTTGCGGGGCGGC-TGGCTTCTTAGGGGGAC
chicken (99) AACTAGTTACCGGAGCCCGAGCGGTCCGGGTCCAACCTCTTAGAGGGAC
wheat (99) AACTAGCTATCCGAG-CCATCCCTCCGCAGC-TAGCTTCTTAGAGGGAC
Consensus (101) AAATAGC GGTGC GCATTTGC GGCCGC T GCTTCTTAGAGGGAC

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GTGGTGCTAGCATTTGCTG Yeast prime up
 CCGCTGGCTTCTTAGGG
 Mold prime up

Figure 7 (continued)

151 200

Z.bali sequencing (121) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
sacc. humal (145) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
cand. coll (145) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
grape (147) TATGCCCGCTTAGGCCAAGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
zygo. ruxil (146) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
PD sequencing (135) TATCGGCT-CAAGCCGATGGAAGTGC CGCGCAATAACAGGTCTGTGATGC
BF sequencing (134) TATCGGCT-CAAGCCGATGGAAGTGC CGCGCAATAACAGGTCTGTGATGC
pen. cry (143) TATCGGCT-CAAGCCGATGGAAGTGC CGCGCAATAACAGGTCTGTGATGC
a. nidu (146) TATCGGCT-CAAGCCGATGGAAGTGC CGCGCAATAACAGGTCTGTGATGC
euro. amst (141) TATCGGCT-CAAGCCGATGGAAGTGC CGCGCAATAACAGGTCTGTGATGC
asp. cand (144) TATCGGCT-CAAGCCGATGGAAGTGC CGCGCAATAACAGGTCTGTGATGC
chicken (149) AAGTCGGCTTACGGC-ACCCGAGATTGAG-CAATAACAGGTCTGTGATGC
wheat (147) TATCGGCTTATAGCGACGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
Consensus (151) TATCGGCT CAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC

201 250

Z.bali sequencing (171) CCTTAGACGTTCTGGGCGGCACGGCGGCTAGACTGACGGAGCCAGCGAGT
sacc. humal (195) CCTTAGACGTTCTGGGCGGCACGGCGGCTAGACTGACGGAGCCAGCGAGT
cand. coll (195) CCTTAGACGTTCTGGGCGGCACGGCGGCTAGACTGACGGAGCCAGCGAGT
grape (197) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGATGTATTCAACGAGT
zygo. ruxil (196) CCTTAGACGTTCTGGGCGGCACGGCGGCTAGACTGACGGAGCCAGCGAGT
PD sequencing (184) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGACAGGGCCAGCGAGT
BF sequencing (183) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGACAGGGCCAGCGGGT
pen. cry (192) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGACAGGGCCAGCGAGT
a. nidu (195) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGACAGGGCCAGCGAGT
euro. amst (190) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGACAGGGCCAGCGAGT
asp. cand (193) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGACAGGGCCAGCGAGT
chicken (197) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGACTGGCTCAGGTTGT
wheat (197) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGATGTATTCAACGAGT
Consensus (201) CCTTAGATGTTCTGGGCGGCACGGCGGCTAGACTGAC GGGCCAGCGAGT

251 300

Z.bali sequencing (221) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGC
sacc. humal (245) CTA-ACCTTGGCCGAGAGGTCTTGGTAATCTTGTGAAACTCCGTCGTGC
cand. coll (245) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGC
grape (247) CTATAGCCTTGGCCGACAGGCCCGGTAATCTTGTGAAACTCCGTCGTGC
zygo. ruxil (246) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGC
PD sequencing (234) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCTGTCGTGC
BF sequencing (233) ACATCACCTTGGCCGAGAGGTCTGGGTAATCTTGTAAACCCTGTCGTGC
pen. cry (242) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCTGTCGTGC
a. nidu (245) ACATCACCTTGGCCGAGAGGCCCGGTAATCTTGTAAACCCTGTCGTGC
euro. amst (240) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCTGTCGTGC
asp. cand (243) ACATCACCTTGGCCGAGAGGTCTGGGTAATCTTGTAAACCCTGTCGTGC
chicken (247) GTCTACCGTACGCCGGCAGGCCCGGTAACCGTTGAACCCCATTCGTGA
wheat (247) ATATAGCCTTGGCCGACAGGCCCGGTAATCTTGGGAAATTTTCATCGTGA
Consensus (251) ATAT ACCTTGGCCGAGAGGTCTGGGTAATCTTGT AAACCC GTCGTGC

GGAGCCAGCGAGTCTAAC Yeast primer low
AGGGCCAGCGAGTACATCA Mold primer low
CGGTTTCAAGCCGATGGAAGT Yeast probe
CTCAAGCCGATGGAAGTGCG Mold probe

Figure 7 (continued)

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301                                350
Z.bali sequencing (269) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
sacc. humal (293) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
cand. coll (293) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
grape (296) TGGGGATA-----
zygo. ruxil (294) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
PD sequencing (284) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
BF sequencing (283) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
pen. cry (292) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
a. nidu (295) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
euro. amst (290) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
asp. cand (293) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
chicken (297) TGGGGATCGGGGATTGCAATTATCCCATGAACGAGGAATTCCTAGTAA
wheat (297) TGGGGATAGATCATTCGCAATTGTTGGTCTTCAACGAGGAATGCCTAGTAA
Consensus (301) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTA

351                                400
Z.bali sequencing (319) GCGCAAGTCATCAACTTGCCTTGATTACGTCCCTGCCCTTTGTACACACA
sacc. humal (343) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
cand. coll (343) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
grape (304) -----
zygo. ruxil (344) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
PD sequencing (334) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACA
BF sequencing (333) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACA
pen. cry (342) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
a. nidu (345) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
euro. amst (340) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
asp. cand (343) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
chicken (347) GTGCGGGTCATAAGCTCGCGTTGATTAAAGTCCCTGCCCTTTGTACACACC
wheat (347) GCGCGAGTCATCAGCTCGCGTTGACTACGTCCCTGCCCTTTGTACACACC
Consensus (351) GC CGAGTCATCAGCTCG G GATTACGTCCCTGCCCTTTGTACACACC

401                                450
Z.bali sequencing (369) AGCCGAAT-----
sacc. humal (393) GCGCGTCGCTAG-----
cand. coll (393) GCGCGTCGCTAGTACC-----
grape (304) -----
zygo. ruxil (394) GCGCGTCGCTAGTA-----
PD sequencing (384) AGCCGA--ATTC-----
BF sequencing (383) AGCCGA--ATTCTGCAGATA-----
pen. cry (392) GCGCGTCGCTACTACCGATTGAATG-----
a. nidu (395) GCGCGTCGCTAC-----
euro. amst (390) GCGCGTCGCTACTACCGATTGAATGGCTCGGTGAGGCC-----
asp. cand (393) GCGCGTCGCTACTACCGATTGAATGGCTCGGTGAGGCCTCCGGACTGGCT
chicken (397) GCGCGTCGCTA-----
wheat (397) GCGCGTCGCTC-----
Consensus (401) GCGCGTCGCTA

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Alignment 2

Alignment Report of Ali 16S alignment.meg ClustaIV (Weighted)
Thursday, September 04, 2003 10:51 AM

1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	Consensus #1	
	G	A	.	G	A	C	Consensus #1
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	Majority	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	43030 16S	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	genbank 16S 43030 AB059664	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	49029 16S	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	genbank 16S 49029 AB042059	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed		
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	genbank 16S 49025 AB042058	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	Clostridium elmenteitii	
1	G	A	G	-	-	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	Geobacillus subterraneus 16S AF276307	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	Sulfobacillus disulfidooxidans 16S U349	
1	G	A	G	A	G	C	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	Bacillus thermoleovorans ribosomal RNA	
	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	Consensus #1
	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	.	A	C	A	T	G	C	A	A	G	T	C	Consensus #1
	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	Majority
30	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	43030 16S
30	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	genbank 16S 43030 AB059664
30	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	49029 16S
30	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	genbank 16S 49029 AB042059
10	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	cc-4902516SRDNA-t7p_C02_006-1-ed
30	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	genbank 16S 49025 AB042058
30	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	C	A	C	A	T	G	C	A	A	G	T	C	Clostridium elmenteitii
29	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	Geobacillus subterraneus 16S AF276307
30	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	Sulfobacillus disulfidooxidans 16S U349
31	T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	Bacillus thermoleovorans ribosomal RNA

Page 2

	60	70	80	90	
	C G G A C - - C . C T T C G G . G - - - - -				Consensus #1
				Consensus #1
	C G G A C - - C - C T T C G G A G - - - - -				Majority
	C G G G T - - C T C T T C G G G A G - - - - -				43030 16S
	C G G G T - - C T C T T C G G G A G - - - - -				genbank 16S 43030 AB059664
	C G G A C - - C - C T T C G G G - G - - - - -				49029 16S
	C G G A C - - C - C T T C G G G - G - - - - -				genbank 16S 49029 AB042059
	C G A G C - - C - C T T C G G G - G - - - - -				cc-4902516SRDNA-t7p_C02_006-1-ed
	C G A G C - - C - C T T C G G G - G - - - - -				genbank 16S 49025 AB042058
	C G G A G T G C C T T T T T G G A C A T T T C C G G A T G G				Clostridium elmentetii
	C G G A C - - C G A A T T G A G A G C T T G C T C T T A T -				Geobacillus subterraneus 16S AF276307
	C G G A C - - T C C T A C G G G A - - - - -				Sulfobacillus disulfidooxidans 16S U349
	- - G A C - - C A A T C C G G A G C T T G C T C T G A T -				Bacillus thermoleovorans ribosomal RNA
	- - - - -				Consensus #1
				Consensus #1
	- - - - -				Majority
	- - - - -				43030 16S
	- - - - -				genbank 16S 43030 AB059664
	- - - - -				49029 16S
	- - - - -				genbank 16S 49029 AB042059
	- - - - -				cc-4902516SRDNA-t7p_C02_006-1-ed
	- - - - -				genbank 16S 49025 AB042058
	- - - - -				Clostridium elmentetii
	A A G A A G A G G T T A C T T T A G C G G G C G G A C C G G G T G				Geobacillus subterraneus 16S AF276307
	- - - - -				Sulfobacillus disulfidooxidans 16S U349
	- - - - -				Bacillus thermoleovorans ribosomal RNA
	- - - - -				43030 16S
	- - - - -				genbank 16S 43030 AB059664
	- - - - -				49029 16S
	- - - - -				genbank 16S 49029 AB042059
	- - - - -				cc-4902516SRDNA-t7p_C02_006-1-ed
	- - - - -				genbank 16S 49025 AB042058
	- - - - -				Clostridium elmentetii
	A A G A A G A G G T T A C T T T A G C G G G C G G A C C G G G T G				Geobacillus subterraneus 16S AF276307
	- - - - -				Sulfobacillus disulfidooxidans 16S U349
	- - - - -				Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)
Thursday, September 04, 2003 10:51 AM

A G T A A C A C G T G G G C A A T C T G C C . . . C A G A C																										Consensus #1						
A G . A A C . C G T G G G . A A . C . . . C C																										Consensus #1						
A G T A A C A C G T G G G C A A T C T G C C T T T C A G A C																										Majority						
93	A	G	G	A	A	C	A	C	G	T	G	G	C	T	A	A	T	C	T	G	C	C	T	T	T	C	A	G	C	43030 16s		
93	A	G	G	A	A	C	A	C	G	T	G	G	C	T	A	A	T	C	T	G	C	C	T	T	T	C	A	G	C	genbank 16s 43030 AB059664		
91	A	G	T	A	A	C	A	C	G	T	G	G	C	T	A	A	T	C	C	A	A	C	C	A	A	C	T	G	A	C	49029 16s	
91	A	G	T	A	A	C	A	C	G	T	G	G	C	T	A	A	T	C	C	C	A	A	C	C	A	A	C	T	G	A	C	genbank 16s 49029 AB042059
71	A	G	T	A	A	C	A	C	G	T	G	G	C	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	cc-4902516SRDNA-t7p_C02_006-1-ed	
91	A	G	T	A	A	C	A	C	G	T	G	G	C	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	genbank 16s 49025 AB042058	
120	A	G	T	A	A	C	A	C	G	T	G	G	C	C	A	A	T	C	T	G	C	C	T	T	G	A	T	C	A	G	Clostridium elmenteitii	
106	A	G	T	A	A	C	A	C	G	T	G	G	C	C	A	A	T	C	T	G	C	C	C	G	C	C	A	A	G	A	C	Geobacillus subterraneus 16S AF276307
93	A	G	G	A	A	C	A	C	G	T	G	G	C	C	C	A	A	T	C	T	G	C	C	C	A	T	G	G	A	C	Sulfobacillus disulfidooxidans 16S U349	
104	A	G	T	A	A	C	A	C	G	T	G	G	C	C	C	C	G	C	A	A	G	A	C	C	G	C	A	A	G	A	C	Bacillus thermoleovorans ribosomal RNA
C G G A A T A A C . C C . G G A A A C G G G T G C T A A T G																										Consensus #1						
. G G . A . A A C . . . G G A A A C . . G . G C T A A . .																										Consensus #1						
C G G A A T A A C G C C C G G A A A C G G G T G C T A A T G																										Majority						
123	C	G	G	A	A	T	A	A	C	G	C	C	C	C	G	G	A	A	C	G	G	G	C	G	C	T	A	A	A	G	43030 16s	
123	C	G	G	A	A	T	A	A	C	G	C	C	C	C	G	G	A	A	C	G	G	G	C	G	C	T	A	A	T	G	genbank 16s 43030 AB059664	
121	C	G	G	A	A	T	A	A	C	G	C	C	C	C	T	G	G	A	A	C	G	G	T	G	C	T	A	A	T	G	49029 16s	
121	C	G	G	A	A	T	A	A	C	G	C	C	C	C	T	G	G	A	A	C	G	G	T	G	C	T	A	A	T	G	genbank 16s 49029 AB042059	
101	T	G	G	A	A	T	A	A	C	A	C	C	C	C	C	T	G	G	A	A	C	G	G	T	G	C	T	A	A	T	G	cc-4902516SRDNA-t7p_C02_006-1-ed
121	T	G	G	A	A	T	A	A	C	A	C	C	C	C	C	T	G	G	A	A	C	G	G	T	G	C	T	A	A	T	G	genbank 16s 49025 AB042058
150	G	G	G	A	A	T	A	A	C	A	C	C	C	C	C	T	G	G	A	A	C	G	G	T	G	C	T	A	A	T	A	Clostridium elmenteitii
136	C	G	G	A	A	T	A	A	C	T	C	C	C	C	C	T	G	G	A	A	C	C	G	A	G	C	T	A	A	T	A	Geobacillus subterraneus 16S AF276307
123	T	G	G	A	A	T	A	A	C	G	C	C	C	C	C	T	G	G	A	A	C	G	G	T	G	C	T	A	A	G	C	Sulfobacillus disulfidooxidans 16S U349
134	C	G	G	A	A	T	A	A	C	T	C	C	C	C	C	T	G	G	A	A	C	C	G	A	G	C	T	A	A	T	A	Bacillus thermoleovorans ribosomal RNA

C	C	G	G	A	T	A	-	-	-	C	.	C	G	A	G	.	A	G	G	C	A	T	C	T	.	C	T	T		Consensus #1
C	C	.	.	A	T	A	-	-	-	G	C	.	T	Consensus #1
C	C	G	G	A	T	A	-	A	C	C	C	G	C	G	A	G	G	A	G	G	C	A	T	C	T	T	C	T	T	Majority

153	C	C	G	G	A	T	A	C	G	C	C	C	G	C	G	A	G	G	A	G	G	C	A	T	C	T	T	C	T	T	43030 16S	
153	C	C	G	G	A	T	A	C	G	C	C	C	G	C	G	A	G	G	A	G	G	C	A	T	C	T	T	C	T	T	genbank 16S 43030 AB059664	
151	C	C	G	G	A	T	A	-	G	G	C	C	A	G	C	G	A	G	C	A	G	C	A	T	C	T	T	C	T	C	49029 16S	
151	C	C	G	G	A	T	A	-	G	G	C	C	A	G	C	G	A	G	C	A	G	C	A	T	C	T	T	C	T	C	genbank 16S 49029 AB042059	
131	C	C	G	G	A	T	A	-	A	T	A	C	C	A	G	G	G	T	A	G	G	C	A	T	C	T	T	C	T	T	cc-4902516SRDNA-t7p_C02_006-1-ed	
151	C	C	G	G	A	T	A	-	A	T	A	C	C	A	G	G	G	T	A	G	G	C	A	T	C	T	T	C	T	T	genbank 16S 49025 AB042058	
180	C	C	G	G	A	T	A	G	C	T	C	T	A	T	A	T	A	T	G	G	C	A	T	C	A	T	G	A	G	G	Clostridium elmenteitii	
166	C	C	G	G	A	T	A	-	A	C	C	A	C	C	G	A	A	G	A	C	C	G	C	A	T	G	G	T	C	T	T	Geobacillus subterraneus 16S AF276307
153	C	C	A	G	A	T	A	G	A	C	A	C	A	-	G	A	A	G	A	G	C	C	T	C	T	C	T	T	G	Sulfobacillus disulfidooxidans 16S U349		
164	C	C	G	G	A	T	A	-	A	C	A	C	C	G	A	A	G	A	C	C	G	C	A	T	G	G	T	C	T	T	Bacillus thermoleovorans ribosomal RNA	

G	.	G	G	.	G	A	A	A	G	G	T	G	-	C	A	A	.	T	G	-	-	.	A	T	C	G	C	T	G		Consensus #1
.	.	.	.	G	.	A	A	G	G	Consensus #1	
G	C	G	G	G	A	A	A	G	G	T	G	-	C	A	A	T	T	G	-	-	-	C	A	T	C	G	C	T	G	Majority	

183	G	C	G	G	G	G	A	A	G	G	C	C	-	C	A	A	T	T	G	-	-	G	G	T	C	G	C	T	G		43030 16S
183	G	C	G	G	G	G	A	A	G	G	C	C	-	C	A	A	T	T	G	-	-	G	G	C	C	G	C	T	G	genbank 16S 43030 AB059664	
180	G	C	T	G	G	A	A	G	G	T	G	-	C	A	A	G	T	G	-	-	-	C	A	C	C	G	C	A	G	49029 16S	
180	G	C	T	G	G	A	A	G	G	T	G	-	C	A	A	A	T	G	-	-	-	C	A	C	C	G	C	A	G	genbank 16S 49029 AB042059	
160	G	T	G	T	T	G	A	A	G	A	T	G	-	C	A	A	C	T	G	-	-	-	C	A	T	C	G	C	T	G	cc-4902516SRDNA-t7p_C02_006-1-ed
180	G	T	G	T	T	G	A	A	G	A	T	G	-	C	A	A	C	T	G	-	-	-	C	A	T	C	G	C	T	G	genbank 16S 49025 AB042058
210	A	T	A	G	A	G	A	A	G	A	T	-	-	T	A	T	C	G	G	-	-	A	T	C	A	-	-	-	-	Clostridium elmenteitii	
195	C	G	G	T	T	G	A	A	G	G	C	G	C	C	T	T	T	G	G	C	T	G	T	C	A	C	T	T	T	Geobacillus subterraneus 16S AF276307	
182	T	G	T	G	G	A	A	A	G	A	T	G	-	C	A	T	C	C	G	-	-	-	C	A	T	G	C	C	A	Sulfobacillus disulfidooxidans 16S U349	
193	T	G	G	T	T	G	A	A	A	G	G	C	G	G	C	-	T	T	T	G	G	C	T	G	A	C	T	T	T	Bacillus thermoleovorans ribosomal RNA	

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)
Thursday, September 04, 2003 10:51 AM

Alignment 2

Page 3

A . . G A G G A G C C C G C G G C G C A T T A G C C T A G T T Consensus #1																															
. . . G A . G . G C C C G C G . C . . A T T A G C C T . G T T Consensus #1																															
A G G G A G G A G C C C G C G G C G C A T T A G C C T A G T T Majority																															
250										260										270											
210	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	A	G	T	T	43030 16S			
210	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	N	G	T	T	genbank 16S 43030 AB059664			
207	A	T	G	G	A	G	A	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	G	G	T	T	49029 16S			
207	A	T	G	G	A	G	A	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	G	G	T	T	genbank 16S 49029 AB042059			
187	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	A	G	T	T	cc-4902516SRDNA-t7p_C02_006-1-ed			
207	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	A	G	T	T	genbank 16S 49025 AB042058			
233	-	-	A	G	A	C	G	A	C	T	G	C	C	C	C	T	G	A	T	A	G	C	C	T	A	G	T	T	Clostridium elmenteitii		
225	G	C	G	G	A	T	G	G	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	A	G	T	T	Geobacillus subterraneus 16S AF276307		
209	G	T	G	G	A	G	A	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	G	G	T	T	Sulfolobacillus disulfidooxidans 16S U349			
222	G	C	G	G	A	T	G	G	C	C	C	G	C	G	C	A	T	T	A	G	C	C	T	A	G	T	T	Bacillus thermoleovorans ribosomal RNA			
G G T G . G G T A A C G G C T C A C C A A G G C C G A C G A T Consensus #1										Consensus #1																					
G G . . . G G T A A C G G . . . A C C A A G G C . . . G A T Consensus #1										Consensus #1																					
G G T G G G T A A C G G C T C A C C A A G G C C G A C G A T Majority										Majority																					
280										290										300											
240	G	G	C	G	G	T	A	A	C	G	G	C	C	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	43030 16S		
240	G	G	C	G	G	T	A	A	C	G	G	C	C	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	genbank 16S 43030 AB059664		
237	G	G	T	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	49029 16S		
237	G	G	T	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	genbank 16S 49029 AB042059		
217	G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	cc-4902516SRDNA-t7p_C02_006-1-ed
237	G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	genbank 16S 49025 AB042058
261	G	G	T	A	A	G	G	T	A	A	C	G	G	C	T	T	A	C	C	A	A	G	G	C	C	T	T	G	A	T	Clostridium elmenteitii
255	G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	Geobacillus subterraneus 16S AF276307
239	G	G	C	G	G	T	A	A	C	G	G	A	C	C	C	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	Sulfolobacillus disulfidooxidans 16S U349
252	G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	Bacillus thermoleovorans ribosomal RNA

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)
Thursday, September 04, 2003 10:51 AM

Alignment 2

Page 0

G C G T A G C C G A C C T G A G A G G G T G A C C G G C C A Consensus #1																															
. . G T A G C C G . C C T G A G A G G G T G . . C G G C C A Consensus #1																															
G C G T A G C C G A C C T G A G A G G G T G A C C G G C C A Majority																															
270	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	43030 16s
270	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	genbank 16s 43030 AB059664
267	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	49029 16s
267	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	genbank 16s 49029 AB042059
247	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	cc-4902516SRDNA-t7p_C02_006-1-ed
267	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	genbank 16s 49025 AB042058
291	C	A	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	Clostridium elmenteitii
285	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	Geobacillus subterraneus 16S AF276307
269	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	Sulfobacillus disulfidooxidans 16S U349
282	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	G	T	G	A	C	C	G	G	C	C	A	Bacillus thermoleovorans ribosomal RNA
C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Consensus #1															Consensus #1																
C A C T G G . A C T G A G A C A C G G . C C A G A C T C C T Consensus #1															Consensus #1																
C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Majority															Majority																
300	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	43030 16s
300	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	genbank 16s 43030 AB059664
297	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	49029 16s
297	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	genbank 16s 49029 AB042059
277	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	cc-4902516SRDNA-t7p_C02_006-1-ed
297	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	genbank 16s 49025 AB042058
321	C	A	C	T	G	G	A	C	T	G	A	G	A	C	A	C	G	G	T	C	C	C	A	G	A	C	T	C	C	T	Clostridium elmenteitii
315	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	Geobacillus subterraneus 16S AF276307
299	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	Sulfobacillus disulfidooxidans 16S U349
312	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	Bacillus thermoleovorans ribosomal RNA

Page 1

[illegible]

G T G A G C G A A G A A G G C C T T C G G G T T G T A A A G Consensus #1																														
G T . A G C G A A G A A G G C C T T C G G G T . G T A A A G Consensus #1																														
G T G A G C G A A G A A G G C C T T C G G G T T G T A A A G Majority																														
430										440										450										
390	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	43030 16s
390	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	genbank 16s 43030 AB059664
387	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	49029 16s
387	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	genbank 16s 49029 AB042059
367	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	cc-4902516SRDNA-t7p_C02_006-1-ed
387	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	genbank 16s 49025 AB042058
411	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	Clostridium elmenteitii
405	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	Geobacillus subterraneus 16S AF276307
389	G	T	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	Sulfobacillus disulfidooxidans 16S U349	
402	G	T	G	A	G	C	G	A	A	G	A	A	G	G	C	C	T	T	C	G	G	T	T	G	T	A	A	A	G	Bacillus thermoleovorans ribosomal RNA
C T C T G T T G C T C G G G A - A G A G C G G C A . G G . G Consensus #1										C T . . G T G G G A G Consensus #1										C T C T G T T G C T C G G G A - A G A G C G G C A A G G G G Majority										
460										470										480										
420	G	T	C	T	G	T	T	G	C	T	C	G	G	G	A	-	A	G	A	G	C	G	C	A	T	G	G	G	G	43030 16s
420	C	T	C	T	G	T	T	G	C	T	C	G	G	G	A	-	A	G	A	G	C	G	C	A	T	G	G	G	G	genbank 16s 43030 AB059664
417	C	T	C	A	G	T	C	A	C	T	C	G	G	G	A	-	A	G	A	G	C	G	C	A	A	G	G	G	G	49029 16s
417	G	T	C	A	G	T	C	A	C	T	C	G	G	G	A	-	A	G	A	G	C	G	C	A	A	G	G	G	G	genbank 16s 49029 AB042059
397	G	T	C	T	G	T	T	G	C	T	C	G	G	G	A	-	A	G	A	G	C	G	A	C	A	A	G	A	G	cc-4902516SRDNA-t7p_C02_006-1-ed
417	C	T	C	T	G	T	T	G	C	T	C	G	G	G	A	-	A	G	A	G	C	G	A	C	A	A	G	A	G	genbank 16s 49025 AB042058
441	C	T	C	T	G	T	C	C	T	A	T	G	G	G	A	A	G	A	A	G	A	G	T	-	-	-	-	-	-	Clostridium elmenteitii
435	C	T	C	T	G	T	T	G	T	G	A	G	G	G	A	C	G	A	A	G	A	G	C	C	G	T	T	T	Geobacillus subterraneus 16S AF276307	
419	C	T	T	A	G	T	C	A	C	T	C	G	G	G	A	-	A	G	A	G	C	G	G	-	G	T	G	G	A	Sulfobacillus disulfidooxidans 16S U349
432	C	T	C	T	G	T	G	T	G	A	A	C	G	G	A	C	G	A	A	G	A	G	C	C	G	T	T	T	Bacillus thermoleovorans ribosomal RNA	

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

. GTGGAAAGC.CC.TG.GAGACGGGTACCGA Consensus #1																													
.....GACGGTACC.. Consensus #1																													
AGTGGAAAGCCCCCTTGCCGAGACGGGTACCGA Majority																													
490										500										510									
449	G	A	T	G	G	A	A	A	G	C	C	C	C	G	T	G	C	G	A	43030 16s									
449	G	A	T	G	G	A	A	A	G	C	C	C	C	N	T	G	C	G	A	genbank 16s 43030 AB059664									
446	A	G	T	G	G	A	A	A	G	C	C	C	C	T	T	G	A	G	A	49029 16s									
446	A	G	T	G	G	A	A	A	G	C	C	C	C	T	T	G	A	G	A	genbank 16s 49029 AB042059									
426	A	G	T	G	G	A	A	A	G	C	T	C	C	T	T	G	T	G	A	cc-4902516SRDNA-t7p_C02_006-1-ed									
446	A	G	T	G	G	A	A	A	G	C	T	C	C	T	T	G	T	G	A	genbank 16s 49025 AB042058									
465	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Clostridium elmenteitii									
465	T	G	A	A	C	A	A	G	G	C	G	G	C	G	C	G	-	G	T	Geobacillus subterraneus 16S AF276307									
447	G	A	G	G	A	A	T	G	C	T	C	C	A	C	C	G	A	G	A	Sulfobacillus disulfidooxidans 16S U349									
462	C	G	A	A	G	A	G	G	C	G	G	C	G	C	G	C	-	G	T	Bacillus thermoleovorans ribosomal RNA									
G . G A G G A A G C C C C G G C T A A C T A C G T G C C A G Consensus #1										Consensus #1																			
. . G A G . A A G C C C C G G C . A A . T A C G T G C C A G Consensus #1										Consensus #1																			
G T G A G G A A G C C C C G G C T A A C T A C G T G C C A G Majority										Majority																			
520										530										540									
479	G	T	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	43030 16s									
479	G	T	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	genbank 16s 43030 AB059664									
476	G	A	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	49029 16s									
476	G	A	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	genbank 16s 49029 AB042059									
456	G	T	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	cc-4902516SRDNA-t7p_C02_006-1-ed									
476	G	T	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	genbank 16s 49025 AB042058									
476	A	G	A	G	G	A	A	A	G	C	C	C	C	C	G	G	C	T	A	Clostridium elmenteitii									
494	A	C	G	A	G	A	A	A	G	C	C	C	C	C	G	G	C	T	A	Geobacillus subterraneus 16S AF276307									
477	G	A	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	Sulfobacillus disulfidooxidans 16S U349									
491	A	C	G	A	G	G	A	A	G	C	C	C	C	C	G	G	C	T	A	Bacillus thermoleovorans ribosomal RNA									

	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Consensus #1		
	C	A	G	C	C	G	C	G	G	T	A	A	.	A	C	G	T	A	G	G	G	G	C	.	A	G	C	G	T	Consensus #1		
	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Majority		
509	C	A	G	C	C	G	C	G	G	T	A	A	A	A	C	G	T	A	G	G	G	G	C	G	A	A	G	C	G	T	43030 16s	
509	C	A	G	C	C	G	C	G	G	T	A	A	A	A	C	G	T	A	G	G	G	G	C	G	A	A	G	C	G	T	genbank 16s 43030 AB059664	
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	A	G	C	G	T	49029 16s	
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	A	G	C	G	T	genbank 16s 49029 AB042059	
486	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	A	G	C	G	T	cc-4902516SRDNA-t7p_C02_006-1-ed	
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	A	G	C	G	T	genbank 16s 49025 AB042058	
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	A	G	C	G	T	Clostridium elmenteitii	
524	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	G	A	A	A	G	C	G	T	Geobacillus subterraneus 16S AF276307
507	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	A	G	C	G	T	Sulfobacillus disulfidooxidans 16S U349	
521	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	G	A	A	A	G	C	G	T	Bacillus thermoleovorans ribosomal RN7
	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Consensus #1	
	T	.	T	C	C	G	G	A	A	T	.	A	.	T	G	G	G	.	C	G	T	A	A	A	G	.	G	.	G	C	Consensus #1	
	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Majority	
539	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	43030 16s	
539	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	genbank 16s 43030 AB059664	
536	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	49029 16s	
536	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	genbank 16s 49029 AB042059	
516	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	G	G	G	T	A	A	A	G	C	G	T	G	C	cc-4902516SRDNA-t7p_C02_006-1-ed	
536	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	genbank 16s 49025 AB042058	
536	T	A	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Clostridium elmenteitii	
554	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Geobacillus subterraneus 16S AF276307	
537	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Sulfobacillus disulfidooxidans 16S U349	
551	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Bacillus thermoleovorans ribosomal RNA	

G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	Consensus #1	
G	.	A	.	G	C	G	G	G	T	C	.	G	.	.	.	G	.	.	.	T	G	A	A	A	G	Consensus #1
G	T	A	G	G	C	G	G	T	T	G	C	G	T	A	A	G	T	C	T	G	G	G	T	G	A	A	A	A	G	Majority	

568	G	T	A	G	G	C	G	G	T	C	G	A	G	C	A	A	G	T	C	T	G	G	A	G	T	G	A	A	A	G	43030 16s	
568	G	T	A	G	G	C	G	G	T	C	G	A	G	C	A	A	G	T	C	T	G	G	A	G	T	G	A	A	A	G	genbank 16s 43030 AB059664	
565	G	T	A	G	G	C	G	G	T	T	G	C	G	T	G	T	C	G	T	C	C	G	G	G	T	G	A	A	A	G	49029 16s	
565	G	T	A	G	G	C	G	G	T	T	G	C	G	T	G	T	C	G	T	C	C	G	G	G	T	G	A	A	A	G	genbank 16s 49029 AB042059	
546	G	T	A	N	G	C	G	G	T	T	G	T	G	T	G	T	A	A	G	T	C	T	G	A	A	T	G	A	A	A	G	cc-4902516SRDNA-t7p_C02_006-1-ed
565	G	T	A	G	G	C	G	G	T	T	G	T	G	T	G	T	A	A	G	T	C	T	G	A	G	T	G	A	A	A	G	genbank 16s 49025 AB042058
565	G	T	A	G	G	C	G	G	C	T	A	A	G	T	A	A	G	T	C	A	G	G	G	T	G	A	A	A	A	G	Clostridium elmenteitii	
583	G	C	A	G	G	C	G	G	T	T	C	T	T	G	T	A	A	G	T	C	T	G	A	T	G	T	G	A	A	A	G	Geobacillus subterraneus 16S AF276307
566	G	T	A	G	G	C	G	G	T	G	T	G	T	G	T	A	A	G	T	C	T	G	A	G	T	G	A	A	A	A	G	Sulfobacillus disulfidooxidans 16S U349
580	G	C	A	G	G	C	G	G	T	T	C	T	T	A	A	G	T	C	T	G	A	T	G	T	G	A	A	A	A	A	G	Bacillus thermoleovorans ribosomal RN

T	C	C	A	.	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	Consensus #1	
.	.	.	.	G	G	C	T	C	.	A	C	C	.	T	C	.	T	T	.	G	A	Consensus #1
T	C	C	A	G	G	C	T	C	A	A	C	C	G	T	G	G	G	A	A	T	G	C	T	T	T	G	G	A	Majority		

598	T	C	C	A	T	G	G	C	T	C	A	A	C	C	A	G	C	A	T	G	G	G	A	T	G	G	G	A	T	G	G	A	43030 16s	
598	T	C	C	A	T	G	G	C	T	C	A	A	C	C	A	A	C	C	A	T	G	G	G	A	T	G	G	G	A	T	G	G	A	genbank 16s 43030 AB059664
595	T	C	C	A	G	G	C	T	C	A	A	C	C	C	C	A	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	49029 16s
595	T	C	C	A	G	G	C	T	C	A	A	C	C	C	C	A	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	genbank 16s 49029 AB042059
576	T	C	C	A	A	G	G	C	T	C	A	A	C	C	C	N	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	cc-4902516SRDNA-t7p_C02_006-1-ed
595	T	C	C	A	A	G	G	C	T	C	A	A	C	C	C	A	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	genbank 16s 49025 AB042058
595	G	C	T	A	C	G	G	C	T	C	A	A	C	C	C	A	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	Clostridium elmenteitii
613	C	C	C	A	C	G	G	C	T	C	A	A	C	C	C	A	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	Geobacillus subterraneus 16S AF276307
596	G	T	C	G	G	C	T	C	A	A	C	C	C	C	C	A	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	Sulfobacillus disulfidooxidans 16S U349
610	C	C	C	A	C	G	G	C	T	C	A	A	C	C	C	A	A	C	C	A	T	G	G	A	T	G	G	G	A	T	G	G	A	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali_16S alignment.meg ClustalV (Weighted)
Thursday, September 04, 2003 10:51 AM

	670	680	690	
628	A A C T G C . T G - A C T T G A G T G C T G G A G A G G C A	C T T G A G T G C T G G A G A G G C A	43030 16S	genbank 16S 43030 AB059664
628	A A C T G C T T G A G T G C . G G A G A G G . .	C T T G A G T G C T G G A G A G G C A	49029 16S	genbank 16S 49029 AB042059
625	A A C T G C G T G - A C T T G A G T G C T G G A G A G G C A	C T T G A G T G C T G G A G A G G C A	cc-4902516SRDNA-t7p_C02_006-1-ed	genbank 16S 49025 AB042058
625	A A C T G C G T G - A C T T G A G T G C T G G A G A G G C A	C T T G A G T G C T G G A G A G G C A	Clostridium elmenteitii	Geobacillus subterraneus 16S AF276307
606	A A C T G C A T G G A C T T G A G T G C C A G G A G A G G C A	C T T G A G T G C C A G G A G A G G C A	Sulfobacillus disulfidooxidans 16S U349	Bacillus thermoleovorans ribosomal RN7
625	A A C T G C A T G G A C T T G A G T G C C A G G A G A G G C A	C T T G A G T G C C A G G A G A G G C A		
624	A A C T G C T T A G - C T T G A G T G C C A G G A G A G G C A	C T T G A G T G C C A G G A G A G G C A		
643	A A C T G - G G G A C T T G A G T G C C A G G A G A G G C A	C T T G A G T G C C A G G A G A G G C A		
626	A A C T G C A A G - A C T T G A G T G C C A G G A G A G G C A	C T T G A G T G C C A G G A G A G G C A		
640	A A C T G - G G G A C T T G A G T G C C A G G A G A G G C A	C T T G A G T G C C A G G A G A G G C A		
	A G G G G A A T T C C A C G T G T - A G C G G T G . A A - T	A G C G G T G . A A - T	Consensus #1	
	A G . . . A A T T C C . . G T G T . A . C G G T G . A A . T	A . C G G T G . A A . T	Consensus #1	
	A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T	Majority	
	670	710	720	
657	A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T	43030 16S	genbank 16S 43030 AB059664
657	A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T	49029 16S	genbank 16S 49029 AB042059
654	A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T	cc-4902516SRDNA-t7p_C02_006-1-ed	genbank 16S 49025 AB042058
654	A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T	Clostridium elmenteitii	Geobacillus subterraneus 16S AF276307
636	A G G C N A A T T C C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T	Sulfobacillus disulfidooxidans 16S U349	Bacillus thermoleovorans ribosomal RNA
654	A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T		
653	A G T G G A A T T C C C T A G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T		
672	A G C G G A A T T C C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T		
655	A G G G G A A T T C C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T		
669	A G C G G A A T T C C C A C G T G T - A G C G G T G A A A - T	A G C G G T G A A A - T		

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

	730	740	750	
685	GCGT - A G A . A T G T G G A G G A A T A C C A G T G G C			43030 16s
685	GCG . . A . A . A T . . G G A G G A A . A C C A G T G G C			genbank 16s 43030 AB059664
682	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			49029 16s
682	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			genbank 16s 49029 AB042059
666	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			cc-4902516SRDNA-t7p_C02_006-1-ed
682	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			genbank 16s 49025 AB042058
681	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			Clostridium elmenteitii
700	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			Geobacillus subterraneus 16S AF276307
683	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			Sulfobacillus disulfidooxidans 16S U34
697	GCGT - A G A T A T G T G G A G G A A T A C C A G T G G C			Bacillus thermoleovorans ribosomal RNA
				Consensus #1
				Consensus #1
				Majority

	760	770	780	
714	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			43030 16s
714	. A A . G C G . C T . . C T G G . C . G			genbank 16s 43030 AB059664
711	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			49029 16s
711	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			genbank 16s 49029 AB042059
696	N A A N G C G C C T T - G C T G G A C A G T G A C T G A C G			cc-4902516SRDNA-t7p_C02_006-1-ed
711	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			genbank 16s 49025 AB042058
710	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			Clostridium elmenteitii
729	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			Geobacillus subterraneus 16S AF276307
712	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			Sulfobacillus disulfidooxidans 16S U349
726	G A A G G C G C C T T - G C T G G A C A G T G A C T G A C G			Bacillus thermoleovorans ribosomal RNA

	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	Consensus #1	
	C	T	G	A	Consensus #1		
	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	Majority	
743	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	43030 16s	
743	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	genbank 16s 43030 AB059664	
740	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	49029 16s	
740	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	genbank 16s 49029 AB042059	
721	C	T	G	A	cc-4902516SRDNA-t7p_C02_006-1-ed		
740	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	genbank 16s 49025 AB042058	
739	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	Clostridium elmenteitii	
758	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	Geobacillus subterraneus 16S AF276307	
741	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	G	T	G	G	G	A	G	C	A	A	A	C	A	G	Sulfobacillus disulfidooxidans 16S U349	
755	C	T	G	A	G	G	C	A	C	G	A	A	A	G	C	T	G	G	G	A	G	C	A	A	A	C	A	C	A	G	Bacillus thermoleovorans ribosomal RNA
	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	Consensus #1
	Consensus #1		
	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	Majority
773	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	43030 16s
773	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	genbank 16s 43030 AB059664
770	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	49029 16s
770	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	genbank 16s 49029 AB042059
725	cc-4902516SRDNA-t7p_C02_006-1-ed		
770	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	genbank 16s 49025 AB042058
768	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	Clostridium elmenteitii
788	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	Geobacillus subterraneus 16S AF276307
771	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	Sulfobacillus disulfidooxidans 16S U349
784	G	A	T	T	A	G	A	T	A	C	C	C	T	G	G	T	A	G	T	C	C	A	C	G	C	C	G	T	A	A	Bacillus thermoleovorans ribosomal RNA

A C G A T G A G T G C T A G G T G T T G G - G G G G T C A C																											Consensus #1				
.																											Consensus #1				
A C G A T G A G T G C T A G G T G T T G G - G G G G T C A C																											Majority				
803	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	T	G	G	-	G	G	G	G	A	C	A	C	43030 16S
803	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	G	A	C	A	C	genbank 16S 43030 AB059664	
800	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	G	T	A	C	C	49029 16S	
800	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	G	T	A	C	C	genbank 16S 49029 AB042059	
725	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
800	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	G	A	C	A	C	genbank 16S 49025 AB042058	
798	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	A		Clostridium elmenteitii	
818	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	T	A	G	A	G	G	G	G	T	C	A	C		Geobacillus subterraneus 16S AF276307	
801	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	G	T	A	C	C		Sulfobacillus disulfidooxidans 16S U349
814	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	T	A	G	A	G	G	G	G	T	C	A	C		Bacillus thermoleovorans ribosomal RNA	
A C C C . C - A G T G C C C G A A G G A A A C C C A A T A A G																											Consensus #1				
. G C . G . A G																											Consensus #1				
A C C C T C - A G T G C C C G A A G G A A A C C C A A T A A G																											Majority				
832	A	C	C	C	-	C	-	A	G	T	G	C	C	G	A	A	C	A	A	M	C	C	C	A	A	T	A	A	G	43030 16S	
832	A	C	C	C	-	C	-	A	G	T	G	C	C	G	A	A	C	C	C	A	A	C	C	C	A	A	T	A	A	G	genbank 16S 43030 AB059664
829	A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	C	C	C	A	A	C	C	C	A	A	T	A	A	G	49029 16S
829	A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	C	C	C	A	A	C	C	C	A	A	T	A	A	G	genbank 16S 49029 AB042059
725	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
829	A	C	C	C	-	C	-	A	G	T	G	C	C	G	A	A	C	C	C	A	A	C	C	C	A	A	T	A	A	G	genbank 16S 49025 AB042058
826	A	C	C	-	-	T	C	A	G	T	G	C	C	G	A	A	C	C	C	A	A	C	C	A	A	T	A	A	A	G	Clostridium elmenteitii
848	A	C	C	C	T	T	A	G	T	G	C	C	T	G	C	A	A	C	C	G	C	G	C	G	A	T	A	A	G	Geobacillus subterraneus 16S AF276307	
830	A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	C	C	C	A	A	C	C	A	A	T	A	A	A	G	Sulfobacillus disulfidooxidans 16S U349
844	A	C	C	C	T	T	A	G	T	G	C	C	T	G	C	A	A	C	C	G	C	G	C	A	T	A	A	A	G	Bacillus thermoleovorans ribosomal RNA	

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Alignment 2

Thursday, September 04, 2003 10:51 AM

C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C																Consensus #1
.																Consensus #1
C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C																Majority
860	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	43030 16S
860	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	genbank 16S 43030 AB059664
858	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	49029 16S
858	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	genbank 16S 49029 AB042059
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
857	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	genbank 16S 49025 AB042058
854	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	Clostridium elmenteitii
878	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	Geobacillus subterraneus 16S AF276307
859	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	Sulfobacillus disulfidooxidans 16S U349
873	C	A	C	T	C	C	G	C	C	T	G	G	G	A	G	Bacillus thermoleovorans ribosomal RNA
T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G																Consensus #1
.																Consensus #1
T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G																Majority
890	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	43030 16S
890	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	genbank 16S 43030 AB059664
888	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	49029 16S
888	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	genbank 16S 49029 AB042059
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
887	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	genbank 16S 49025 AB042058
884	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	Clostridium elmenteitii
908	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	Geobacillus subterraneus 16S AF276307
889	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	Sulfobacillus disulfidooxidans 16S U349
903	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of All 16S alignment.meg ClustalV (Weighted)
Thursday, September 04, 2003 10:51 AM

	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Consensus #1	
	Consensus #1	
	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Majority
919	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	43030 16s
919	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	genbank 16s 43030 AB059664
917	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	49029 16s
917	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	genbank 16s 49029 AB042059
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
916	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	genbank 16s 49025 AB042058
914	C	A	C	A	A	G	C	A	G	C	A	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Clostridium elmenteitii
937	C	A	C	A	A	G	C	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Geobacillus subterraneus 16S AF276307	
918	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Sulfobacillus disulfidooxidans 16S U349
932	C	A	C	A	A	G	C	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Bacillus thermoleovorans ribosomal RN7	
	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Consensus #1
	Consensus #1	
	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Majority
949	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	43030 16s
949	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	genbank 16s 43030 AB059664
947	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	C	G	49029 16s
947	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	genbank 16s 49029 AB042059
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
946	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	genbank 16s 49025 AB042058
944	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Clostridium elmenteitii
967	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	T	T	T	G	Geobacillus subterraneus 16S AF276307
948	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Sulfobacillus disulfidooxidans 16S U349
962	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	T	T	T	G	Bacillus thermoleovorans ribosomal RNA

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Alignment 2

Thursday, September 04, 2003 10:51 AM

A C A T C C C . C T G A C A . C C . . A G A G A T - - - G C Consensus #1																																
. C A G A G A T - - - G C Consensus #1																																
A C A T C C C C T C T G A C A G C C G C A G A G A T - - - G C Majority																																
1030										1040								1050														
979	A	C	A	T	C	C	C	C	T	C	T	G	A	C	A	C	C	T	C	A	G	A	G	A	T	-	-	G	A	43030 16s		
979	A	C	A	T	C	C	C	T	C	T	G	A	C	A	C	C	C	T	C	A	G	A	G	A	T	-	-	G	A	genbank 16s 43030 AB059664		
977	A	C	A	T	C	C	C	C	C	T	G	A	C	A	G	C	C	G	C	A	G	A	G	A	T	-	-	G	C	49029 16s		
977	A	C	A	T	C	C	C	C	T	G	A	C	A	G	C	C	G	C	A	G	A	G	A	T	-	-	G	C	genbank 16s 49029 AB042059			
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed		
976	A	C	A	T	C	C	C	T	C	T	G	A	C	C	G	G	T	G	C	A	G	A	G	A	T	-	-	G	T	genbank 16s 49025 AB042058		
974	A	C	A	T	C	C	C	T	C	T	G	A	C	C	G	T	G	A	G	T	A	A	-	-	-	-	-	G	T	C	Clostridium elmentarii	
997	A	C	A	T	C	C	C	-	C	T	G	A	C	A	C	C	C	A	A	G	A	G	A	T	T	G	G	G	C	C	Geobacillus subterraneus 16S AF276307	
978	A	C	A	T	C	C	C	C	C	A	G	A	C	G	G	T	G	T	A	G	A	G	A	T	-	-	-	A	C	C	Sulfobacillus disulfidooxidans 16S U349	
992	A	C	A	T	C	C	C	-	C	T	G	A	C	A	C	C	C	A	A	G	A	G	A	T	T	G	G	G	C	C	C	Bacillus thermoleovorans ribosomal RNA
G . . . T C C C T T C G G G G C A G - - . G G A G A C A G G Consensus #1																																
. C A G A G A T - - - G C Consensus #1																																
G G T T T C C C C T T C G G G G C A G - - G G G A G A C A G G Majority																																
1060										1070								1080														
1006	G	G	G	T	C	C	C	T	T	C	G	G	G	G	C	A	G	-	-	A	G	G	A	G	A	C	A	G	G	43030 16s		
1006	G	G	G	T	C	C	C	T	T	C	G	G	G	G	C	A	G	-	-	A	G	G	A	G	A	C	A	G	G	genbank 16s 43030 AB059664		
1004	G	G	T	T	C	C	C	T	T	C	G	G	G	G	C	A	G	-	-	G	G	G	A	G	A	C	A	G	G	49029 16s		
1004	G	G	T	T	C	C	C	T	T	C	G	G	G	G	C	A	G	-	-	G	G	G	A	G	A	C	A	G	G	genbank 16s 49029 AB042059		
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed		
1003	A	C	C	T	T	C	C	C	T	T	C	G	G	G	G	C	A	G	-	-	A	G	G	A	G	A	C	A	G	G	genbank 16s 49025 AB042058	
1001	A	C	C	T	T	C	C	C	T	T	C	G	G	G	G	A	C	A	G	-	-	A	G	G	A	G	A	C	A	G	G	Clostridium elmentarii
1026	G	T	T	C	C	C	C	T	T	C	G	G	G	G	G	G	A	C	A	G	G	G	T	G	A	C	A	G	G	C	Geobacillus subterraneus 16S AF276307	
1005	A	C	C	G	T	C	C	C	T	T	C	G	G	G	G	C	T	G	-	-	G	G	G	A	G	A	C	A	G	G	C	Sulfobacillus disulfidooxidans 16S U349
1021	G	T	T	C	C	T	T	C	-	-	-	-	-	-	-	-	-	-	-	-	G	G	G	G	A	C	A	G	A	G	C	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Page 19

	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Consensus #1
	Consensus #1
	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Majority
	1090										1100										1110										
1034	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	43030 16S
1034	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	genbank 16S 43030 AB059664
1032	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	49029 16S
1032	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	genbank 16S 49029 AB042059
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1031	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	genbank 16S 49025 AB042058
1029	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Clostridium elmentarii
1056	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Geobacillus subterraneus 16S AF276307
1033	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Sulfobacillus disulfidooxidans 16S U349
1047	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Bacillus thermoleovorans ribosomal RNA
	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Consensus #1
	Consensus #1	
	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Majority
	1120										1130										1140										
1064	G	A	G	A	T	G	T	T	G	G	G	T	T	C	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	43030 16S
1064	G	A	G	A	T	G	T	T	G	G	G	T	T	C	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	genbank 16S 43030 AB059664
1062	G	A	G	A	T	G	T	T	G	G	G	T	T	C	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	49029 16S
1062	G	A	G	A	T	G	T	T	G	G	G	T	T	C	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	genbank 16S 49029 AB042059
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1061	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	genbank 16S 49025 AB042058
1059	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Clostridium elmentarii
1086	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Geobacillus subterraneus 16S AF276307
1063	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Sulfobacillus disulfidooxidans 16S U349
1077	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

C A A C C C T T G A . C T G T G T T A C C A G C A C G T . . Consensus #1																															
. Consensus #1																															
C A A C C C T T G A C C C T G T G T T A C C A G C A C G T T A Majority																															
1094	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	T	A	C	C	A	G	C	G	C	G	T	T	G	43030 16s		
1094	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	T	A	C	C	A	G	C	G	C	G	T	T	G	genbank 16s 43030 AB059664		
1092	C	A	A	C	C	C	T	T	G	A	A	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	G	49029 16s	
1092	C	A	A	C	C	C	T	T	G	A	A	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	G	genbank 16s 49029 AB042059	
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed		
1091	C	A	A	C	C	C	T	T	G	A	T	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	A	G	genbank 16s 49025 AB042058
1089	C	A	A	C	C	C	T	T	G	A	T	C	A	T	G	T	T	G	C	C	A	G	C	A	T	-	T	T	C	Clostridium elmenteitii	
1116	C	A	A	C	C	C	T	T	G	A	C	T	C	T	A	G	T	T	G	C	C	A	G	C	A	T	T	-	C	Geobacillus subterraneus 16S AF276307	
1093	C	A	A	C	C	C	T	T	G	A	T	C	G	T	G	T	T	A	C	C	A	G	C	G	C	G	T	A	A	Sulfobacillus disulfidooxidans 16S U349	
1107	C	A	A	C	C	C	T	T	G	A	C	T	C	T	A	G	T	T	G	C	C	A	G	C	A	C	G	-	A	Bacillus thermoleovorans ribosomal RNA	
A G G T G G G G A C T C A C A G G T G A C T G C C G G C G - Consensus #1																															
. . . G G G . A Consensus #1																															
A G G T G G G G A C T C A C A G G T G A C T G C C G G C G - Majority																															
1124	A	G	G	C	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	43030 16s
1124	A	G	G	C	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16s 43030 AB059664
1122	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	T	T	G	A	C	T	G	C	C	G	G	C	G	-	49029 16s
1122	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	T	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16s 49029 AB042059
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1121	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16s 49025 AB042058
1118	G	A	T	G	G	G	C	A	C	T	C	T	A	A	T	G	A	G	A	C	T	G	C	C	G	G	T	G	A	Clostridium elmenteitii	
1144	A	G	T	G	G	G	C	A	C	T	C	T	A	G	A	G	G	A	C	T	G	C	C	G	G	C	G	A	Geobacillus subterraneus 16S AF276307		
1123	A	G	G	C	G	G	G	A	C	T	C	A	C	A	G	T	G	A	C	T	G	C	C	G	T	C	G	-	Sulfobacillus disulfidooxidans 16S U349		
1135	A	G	G	T	G	G	G	C	A	C	T	C	T	A	G	A	G	G	A	C	T	G	C	C	G	G	T	G	A	Bacillus thermoleovorans ribosomal RNA	

T A A G T C G G A G G A A G G C G G G G A T G A C G T C A A Consensus #1																									Consensus #1																																																	
T A A G T C G G A G G A A G G C G G G G A T G A C G T C A A Majority																									Majority																																																	
1210																									1220																									1230																								
1153	T	A	A	G	T	C	G	G	A	G	G	A	A	G	G	C	G	G	G	G	A	T	G	A	C	G	T	C	A	A	43030 16S																																											
1153	T	A	A	G	T	C	G	G	A	G	G	A	A	G	G	C	G	G	G	G	A	T	G	A	C	G	T	C	A	A	genbank 16s 43030 AB059664																																											
1151	T	A	A	G	T	C	G	G	A	G	G	A	A	G	G	C	G	G	G	G	A	T	G	A	C	G	T	C	A	A	49029 16s																																											
1151	T	A	A	G	T	C	G	G	A	G	G	A	A	G	G	C	G	G	G	G	A	T	G	A	C	G	T	C	A	A	genbank 16s 49029 AB042059																																											
752	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed																																											
1150	T	A	A	G	T	C	G	G	A	G	G	A	A	G	G	C	G	G	G	G	A	T	G	A	C	G	T	C	A	A	genbank 16s 49025 AB042058																																											
1148	C	A	A	C	C	G	A	G	A	A	G	G	T	G	G	G	G	A	T	G	A	C	G	T	C	A	A	Clostridium elmenteitii																																														
1174	A	A	A	G	T	C	G	G	A	G	A	A	G	G	T	G	G	G	A	T	G	A	C	G	T	C	A	A	Geobacillus subterraneus 16S AF276307																																													
1152	T	A	A	G	A	C	G	G	A	G	A	A	G	G	C	G	G	G	G	A	T	G	A	C	G	T	C	A	A	Sulfobacillus disulfidooxidans 16S U349																																												
1165	C	A	A	G	T	C	G	G	A	G	A	A	G	G	T	G	G	G	G	A	T	G	A	C	G	T	C	A	A	Bacillus thermoleovorans ribosomal RNA																																												
A T C A T C A T G C C C C C T T A T G T C C C T G G G C T A C A Consensus #1																									Consensus #1																																																	
A T C A T C A T G C C C C C T T A T G T C C C T G G G C T A C A Majority																									Majority																																																	
1240																									1250																									1260																								
1183	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	G	A	T	G	T	C	C	C	T	G	G	G	C	T	A	C	A	43030 16s																																									
1183	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	G	A	T	G	T	C	C	C	T	G	G	G	C	T	A	C	A	genbank 16s 43030 AB059664																																									
1181	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	T	A	T	G	T	C	C	C	T	G	G	G	C	T	A	C	A	49029 16s																																									
1181	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	T	A	T	G	T	C	C	C	T	G	G	G	C	T	A	C	A	genbank 16s 49029 AB042059																																									
752	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed																																											
1180	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	T	A	T	G	T	C	C	C	T	G	G	G	C	T	A	C	A	genbank 16s 49025 AB042058																																									
1178	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	T	A	T	G	T	C	C	C	T	G	G	G	C	T	A	C	A	Clostridium elmenteitii																																									
1204	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	T	A	T	G	A	C	C	C	T	G	G	G	C	T	A	C	A	Geobacillus subterraneus 16S AF276307																																									
1182	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	T	A	T	G	T	C	C	C	T	G	G	G	C	T	A	C	A	Sulfobacillus disulfidooxidans 16S U349																																									
1195	A	T	C	A	T	C	A	T	G	C	C	C	C	C	T	T	A	T	G	A	C	C	C	T	G	G	G	C	T	A	C	A	Bacillus thermoleovorans ribosomal RNA																																									

Alignment 2

Alignment Report of Ali_16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

C A C G T G C T A C A A T G G G C G G T A C A A . G G G A . Consensus #1																															
. C A A . . G G . . Consensus #1																															
C A C G T G C T A C A A T G G G C G G T A C A A C G G G A A Majority																															
1270										1280										1290											
1213	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	A	A	A	G	G	G	A	G	43030 16s
1213	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	A	A	A	G	G	G	A	G	genbank 16s 43030 AB059664
1211	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	C	G	G	G	A	A	49029 16s
1211	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	C	G	G	G	A	A	genbank 16s 49029 AB042059
752	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	A	A	C	N	G	G	A	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1210	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	C	G	G	G	A	A	genbank 16s 49025 AB042058
1208	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	C	G	A	T	A	C	A	A	A	G	G	G	C	A	Clostridium elmenteitii	
1234	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	A	G	G	G	C	T	Geobacillus subterraneus 16S AF276307
1212	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	C	A	C	A	A	C	G	G	G	A	C	Sulfobacillus disulfidooxidans 16S U349
1225	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	A	G	G	G	C	T	Bacillus thermoleovorans ribosomal RNA
G C G A A . C C G C G A G G . G G A G C . A A . C C C A . A Consensus #1																															
. Consensus #1																															
G C G A A G C C G C G A G G T G G A G C G A A C C C C A A A Majority																															
1300										1310										1320											
1243	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	G	A	G	C	G	A	A	A	C	C	C	A	A	A	43030 16s	
1243	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	G	A	G	C	G	A	A	A	C	C	C	A	A	A	genbank 16s 43030 AB059664	
1241	G	C	G	A	A	G	C	C	G	C	G	A	G	G	T	G	G	A	G	C	A	A	A	C	C	C	C	T	G	A	49029 16s
1241	G	C	G	A	A	G	C	C	G	C	G	A	G	G	T	G	G	A	G	C	A	A	A	C	C	C	C	T	G	A	genbank 16s 49029 AB042059
760	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1240	G	C	G	A	A	G	C	C	G	C	G	A	G	G	T	G	G	A	G	C	A	A	A	C	C	T	A	A	A	genbank 16s 49025 AB042058	
1238	G	C	G	A	A	G	C	A	G	A	T	C	C	G	G	A	G	C	G	A	A	C	C	C	C	A	T	A	Clostridium elmenteitii		
1264	G	C	G	A	A	C	C	G	C	G	A	G	G	G	G	A	G	C	G	A	A	T	C	C	C	C	A	A	A	Geobacillus subterraneus 16S AF276307	
1242	G	C	G	A	A	G	A	G	C	A	A	T	C	T	G	G	A	G	C	A	C	C	C	C	C	T	G	A	Sulfobacillus disulfidooxidans 16S U349		
1255	G	C	G	A	A	C	C	C	G	C	G	A	G	G	G	G	A	G	C	G	A	A	T	C	C	C	A	A	A	Bacillus thermoleovorans ribosomal RNA	

Alignment 2

Page 23

AAGCCG.TCGTAGTTCGGATTTCGGAATTGCAGGCTGC																										Consensus #1									
.....T.....																										Consensus #1									
AAGCCGCTCGTAGTTCGGATTTCGCAAGGCTGC																										Majority									
1330													1340													1350									
1273	A	A	G	C	C	G	C	T	C	G	T	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	43030 16s				
1273	A	A	G	C	C	G	C	T	C	G	T	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	genbank 16s 43030 AB059664				
1271	A	A	G	C	C	G	T	T	C	G	T	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	49029 16s				
1271	A	A	G	C	C	G	T	T	C	G	T	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	genbank 16s 49029 AB042059				
760	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed				
1270	A	A	G	C	C	G	T	T	C	G	T	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	genbank 16s 49025 AB042058				
1268	A	A	G	T	C	G	T	C	C	A	G	T	T	C	G	G	A	T	T	G	A	G	G	G	C	T	G	C	C	C	Clostridium elmenteitii				
1294	A	A	G	C	C	G	C	T	C	T	C	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	Geobacillus subterraneus 16S AF276307				
1272	A	A	C	C	G	C	T	C	G	T	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	C	Sulfobacillus disulfidooxidans 16S U349				
1285	A	A	G	C	C	G	C	T	C	T	C	A	G	T	T	C	G	G	A	T	T	G	C	A	G	G	C	T	G	C	Bacillus thermoleovorans ribosomal RNA				
A A C T C G C C T G C A T G A A G C C C G G A A T T G C T A G																										Consensus #1									
.....																										Consensus #1									
A A C T C G C C T G C A T G A A G C C C G G A A T T G C T A G																										Majority									
1360													1370													1380									
1303	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	T	G	C	T	A	G	43030 16s				
1303	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	T	G	C	T	A	G	genbank 16s 43030 AB059664				
1301	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	T	G	C	T	A	G	49029 16s				
1301	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	T	G	C	T	A	G	genbank 16s 49029 AB042059				
765	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed				
1300	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	T	G	C	T	A	G	genbank 16s 49025 AB042058				
1298	A	A	C	T	C	G	C	C	C	C	A	T	G	A	A	G	T	T	G	G	A	G	T	T	G	C	T	A	G	C	Clostridium elmenteitii				
1324	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	C	G	C	T	A	G	Geobacillus subterraneus 16S AF276307				
1302	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	T	G	C	T	A	G	Sulfobacillus disulfidooxidans 16S U349				
1315	A	A	C	T	C	G	C	C	T	G	C	A	T	G	A	A	G	C	C	G	G	A	A	T	C	G	C	T	A	G	Bacillus thermoleovorans ribosomal RNA				

Alignment 2

	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	Consensus #1	
	Consensus #1	
	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	Majority
1333	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	43030 16s
1333	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	genbank 16s 43030 AB059664
1331	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	49029 16s
1331	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	genbank 16s 49029 AB042059
765	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1330	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	genbank 16s 49025 AB042058
1328	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	G	Clostridium elmenteitii
1354	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	Geobacillus subterraneus 16S AF276307
1332	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	Sulfobacillus disulfidooxidans 16S U349
1345	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	Bacillus thermoleovorans ribosomal RNA
	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Consensus #1	
	.	.	T	.	C	C	C	Consensus #1		
	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Majority	
1363	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	43030 16s	
1363	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	genbank 16s 43030 AB059664	
1361	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	49029 16s	
1361	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	genbank 16s 49029 AB042059	
765	-	-	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	cc-4902516SRDNA-t7p_C02_006-1-ed
1360	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	genbank 16s 49025 AB042058	
1358	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Clostridium elmenteitii	
1384	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Geobacillus subterraneus 16S AF276307	
1362	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Sulfobacillus disulfidooxidans 16S U349	
1375	C	G	T	T	C	C	C	G	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Bacillus thermoleovorans ribosomal RNA	

Alignment 2

Page 25

A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										Consensus #1
.										Consensus #1
A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										Majority
A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										43030 16s
A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										genbank 16s 43030 AB059664
A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										49029 16s
A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										genbank 16s 49029 AB042059
										cc-4902516SRDNA-t7p_C02_006-1-ed
A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										genbank 16s 49025 AB042058
A C A C C A C G A G A G T C G G G A A G A C C C G A A G C C										Clostridium elmenteitii
A C A C C A C G A G A G T C T T G C A A C A C C C G A A G T C										Geobacillus subterraneus 16S AF276307
A C A C C A C G A G A G T C G A C A A C A C C C G A A G T C										Sulfobacillus disulfidooxidans 16S U349
A C A C C A C G A G A G C T C G C A A C A C C C C										Bacillus thermoleovorans ribosomal RNA
G G T G . G G T A A C C C . T . . . G G G . G C C A G C C G										Consensus #1
.										Consensus #1
G G T G A G G T A A C C C G T G T A G G G A G C C A G C C G										Majority
G G T G A G G T A A C C C C C T G T G G G G A G C C A G C C G										43030 16s
G G T G A G G T A A C C C C C T G T G G G G A G C C A G C C G										genbank 16s 43030 AB059664
G G T G G G G T A A C C C C G T - C A G G G A G C C A G C C G										49029 16s
G G T G G G G T A A C C C C G T - C A G G G G G C C A G C C G										genbank 16s 49029 AB042059
										cc-4902516SRDNA-t7p_C02_006-1-ed
G G T G A G G T A A C C C - G T - T A T G G A G C C A G C C G										genbank 16s 49025 AB042058
C G T A C C G A A C C C T T C G G A C G G - - A A C G G										Clostridium elmenteitii
G G T G A G G T A A C C C C T T A C - G G G A G C C A G C C G										Geobacillus subterraneus 16S AF276307
G G T G G G G T A A C C C C G T A - A G G G G G C C A G C C G										Sulfobacillus disulfidooxidans 16S U349
										Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)
Thursday, September 04, 2003 10:51 AM

	C	C	G	A	A	G	G	T	G	G	G	.	.	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	Consensus #1							
	Consensus #1							
	C	C	G	A	A	G	G	T	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	A	A	G	Majority								
											1510											1520											1530			
1453	C	C	G	A	A	G	G	T	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G						43030 16s						
1453	C	C	G	A	A	G	G	T	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G						genbank 16s 43030 AB059664						
1450	C	C	G	A	A	G	G	T	T	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G						49029 16s						
1450	C	C	G	A	A	G	G	T	T	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G						genbank 16s 49029 AB042059						
770	cc-4902516SRDNA-t7p_C02_006-1-ed																																			
1448	C	C	G	A	A	G	G	T	T	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G						genbank 16s 49025 AB042058						
1445	T	C	G	A	A	G	T	G	A	G	C	C	G	A	T	A	C	T	G	G	G	T	G	A	A	G						Clostridium elmenteitii				
1473	C	C	G	A	A	G	T	G	G	G	C	A	A	G	T	G	A	T	T	G	G	G	T	G	A	A	G						Geobacillus subterraneus 16S AF276307			
1451	C	C	G	A	A	G	T	G	G	G	C	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G						Sulfobacillus disulfidooxidans 16S U349			
1428	Bacillus thermoleovorans ribosomal RNA																																			
	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	Consensus #1							
	Consensus #1								
	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	X	X	X	X	X	X	X	X	X	X	Majority							
											1540											1550											1560			
1483	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T																		43030 16s
1483	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	C	C	G	G	A	A	G	G	T	G	C	genbank 16s 43030 AB059664					
1480	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T																		49029 16s
1480	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	T	C	G	G	A	A	G	G	T	G	C	genbank 16s 49029 AB042059					
770	cc-4902516SRDNA-t7p_C02_006-1-ed																																			
1478	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	T	C	G	G	A	A	G	G	T	G	C	genbank 16s 49025 AB042058					
1475	T	C	G	T	A	A	C	A	A	G	G	T	A	T	C	C	G	T																		Clostridium elmenteitii
1503	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	C	C	G	G	A	A	G	G	T	G	C	Geobacillus subterraneus 16S AF276307					
1481	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T																		Sulfobacillus disulfidooxidans 16S U349
1428	Bacillus thermoleovorans ribosomal RNA																																			

Alignment Report of All 16S alignment.meg ClustalV (Weighted)
Thursday, September 04, 2003 10:51 AM

Alignment 2

Page 27

1500	Consensus #1
1513	Consensus #1
1497	X X X X X X X X X X X X X	Majority
1510		43030 16S
770		genbank 16S 43030 AB059664
1508		49029 16S
1492		genbank 16S 49029 AB042059
1533		cc-4902516SRDNA-t7p_C02_006-1-ed
1496		genbank 16S 49025 AB042058
1428		Clostridium elmenteiitii
		Geobacillus subterraneus 16S AF276307
		Sulfobacillus disulfidooxidans 16S U345
		Bacillus thermoleovorans ribosomal RNA

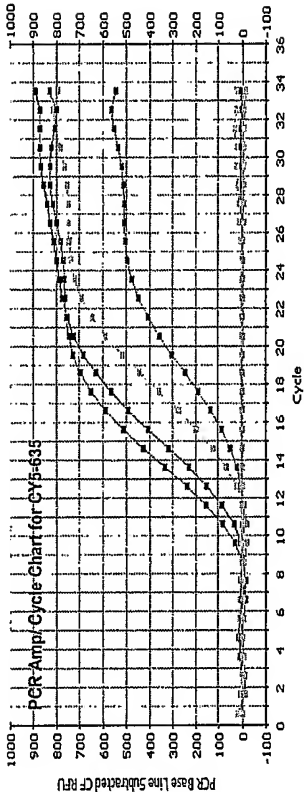
Consensus 'Consensus #1': When 60% (6) match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the consensus named 'Consensus #1' exactly.

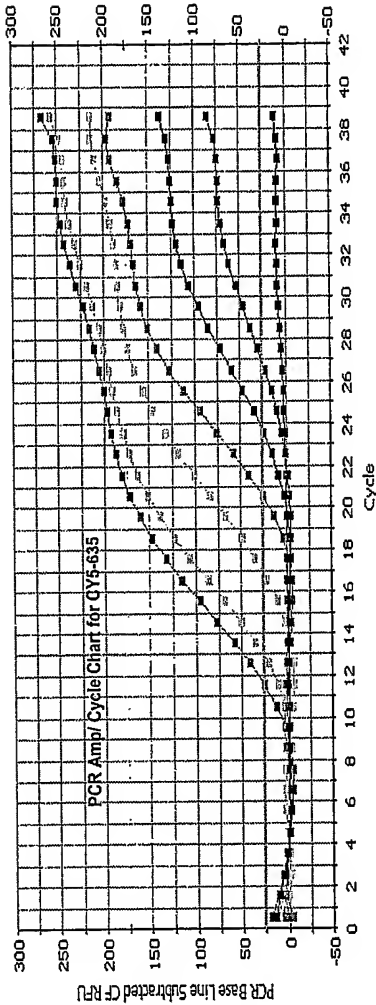
Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Figure 9

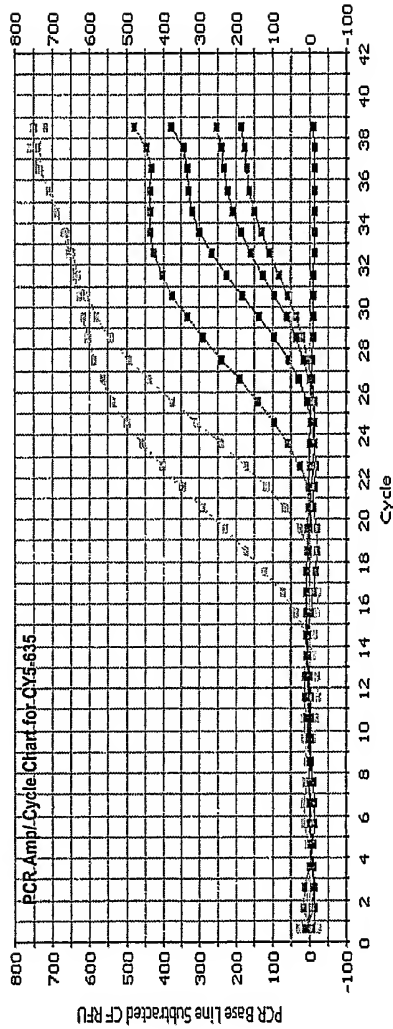


In addition, *G. stearo**thermophilus* can be seen in green. Other curves below the base line include the blank control (red) and the tests for *Lactococcus lactis* C2 (a. blue), *P. putida* 49L/51 (purple) and *E. coli* DH5 α (orange) using the same primer and probe set.

Figure 10



. Dilutions 10^0 (red), 10^{-1} (orange), 10^{-2} (light blue), 10^{-3} (purple), 10^{-4} (black), and 10^{-5} (blue) can be seen above the baseline. The blank control (brown) is below the baseline.



Dilutions 10^{-1} (orange), 10^{-2} (blue), 10^{-3} (purple), 10^{-4} (black), 10^{-5} (blue), and 10^{-6} (green) can be seen above the baseline. The blank control (red) is below the baseline.

5

Figure 11

Figure 12

Zygosaccaromyces

```

5  ATTGGGCCCTCTANAGCATGCTCGACGGCCGCAGTGTGATGGATATCTGCAGAAATTCGGCTTTGCATGGCCGTTCTTAG
   TTGGTGGAGTGATTTGTCTGTCTTAATTGCGATAACGAACGAGACCCTTAACCTACTAAATAGTGGTGTAGCATTTGCTGG
   TTTTCCACNNTTCTTAGAGGACTATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGA
   CGTTCITGGCCGCACGCGGCTACACTGACGGAGCCAGCGAGTCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAA
   CTCCTGTCGTGGGATAGAGCATTTGTAATTATTGCTCTTCAACGAGGAAATCTAGTAAGCGCAAGTCATCAACTTGC
   GTTGATTACGTCCCTGCCCTTTGTACACACAAGCCGAATTCACAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGG
10  TACCAAGCTTGGCGTAATCATGGTCAATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAATTCACACACATACGA
   GCCGAAGCATAAAGTAAAGCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGTCTCACTGCCCGC
   TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAATTAATGAATCGGCCAACGCGCGGGGAGAGCGGTTTGCGTATTGGGC
   GCTCTTCCGCTTCCCTCGCTCACTGACTCGCTCGGTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG
   GTAATAACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCANANGCCAGANCCGT
15  AAAAGCCGCGTGTGGCGTTTTCNNTANGCTCGCCCCCTGACAGCATNCAAAATCGACGCTCAGTCNNANGTGGCGAAC
   CCGNNGGANATAAGATACNNGCGTTNCCCCCTGNANCTCNCTGCGTNTCNNGTNCNANGNCGNTANGGAANCTGNCNC
   CTTTCNCCCTTNGGAACNGGNNCTTNNNNNNNANCNNGNNGNNNNNNNNNGNNN

```

Figure 13

Penicillium digitatum
 5 GANGNCNNCCNNANTNNAATCCTNAGCNGAGTNGNNAAGCGNCGTTCNCCGANGGAGAAAGNGGACAGGTNTCCGTANCGC
 AGGTNNGANCAGGAGAGCGCACGAGGGAGCTNCAGGGGAAAACGCCCTGGGATCTTNA TAGTCNNGT'CGGGTTCNCCACNT
 CTGACTTGAGCGTCGAATTTTGTGATGCTCGTCAGGGGGCGGAGCNTATGGAAAACGCCAGCAACGCGGCCCTTTTACGGTT
 CCTGGCNTTTGCTGGCCCTTTTGTCTCACAATGTTCTTCCCTGCTATCCCTGATTTCTGTGGATAACCGTATTTACCGCCTT
 TGAGTGAGCTGATACCGCTCGCCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGGCCCAA
 10 TAGCAAACCGCCTCTCCCGCGCGTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAAGCGGGC
 AGTGAGCGCAACGCAATTAAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTTACATTTATGCTTCCGGCTCGTAT
 GTTGTGTGGAATTGTAGCGGATAACAATTTCAACAAGGAAA CAGCTATGACCATGATTACGCCAAGCTTGGTACCGAGC
 TCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGGCTTTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCT
 GCTTAATTGCCGATAACGAACGAGACCTCGGCCCTTAAATAGCCCGGTCCGCATTTGGGGCCGCTGGCTTCTTAAGGGGA
 15 CTATCGGCTCAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTGGGCCGACCGCGGCTA
 CACTGACAGGGCCAGCGAGTACATCACCTTAACCGAGAGGTTTGGGTAATCTTGTAAACCCCTGTGTCGTGGGGATAGA
 GCATTGCAATTATTGCTCTTCAACGAGGAATGCCCTAGTAGGCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTT
 TGTACACAAGCCGAATTCTGCAGATATCCATCACACTGGCGGCCGTCGAGCATGCTNTAGAGGGCCCAAT

Byssochlamys fulva

[illegible]

Figure 15
PCR Amp/Cycle Graph for FAM-490

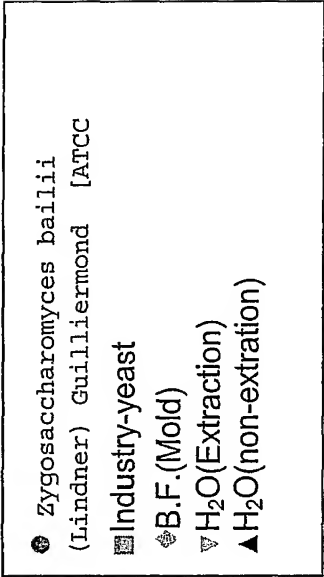
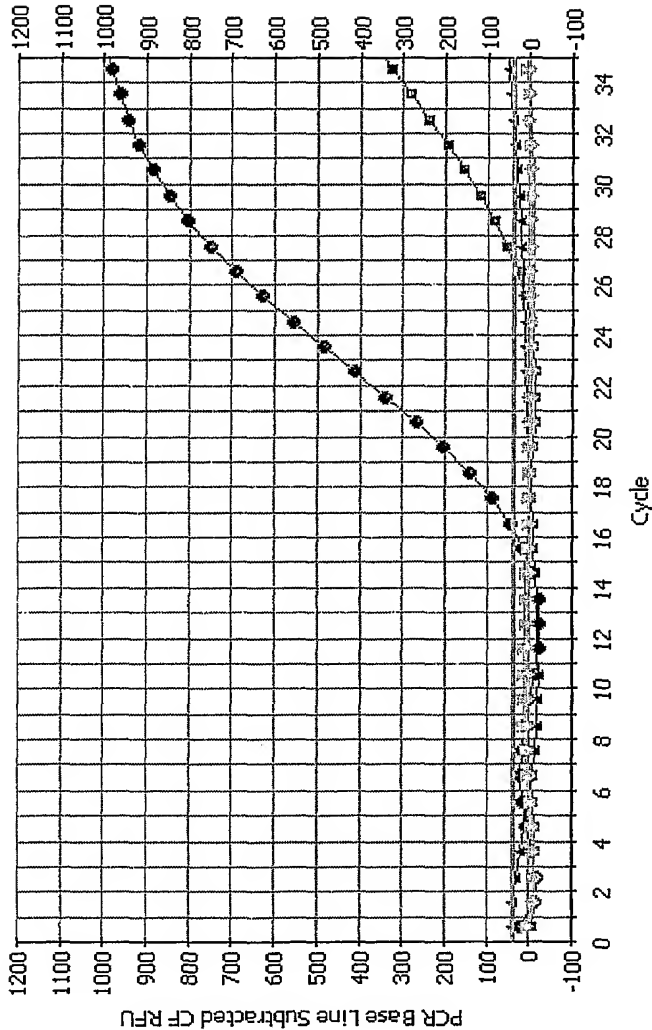


Figure 16
PCR Amp/Cycle Graph for FAM-490

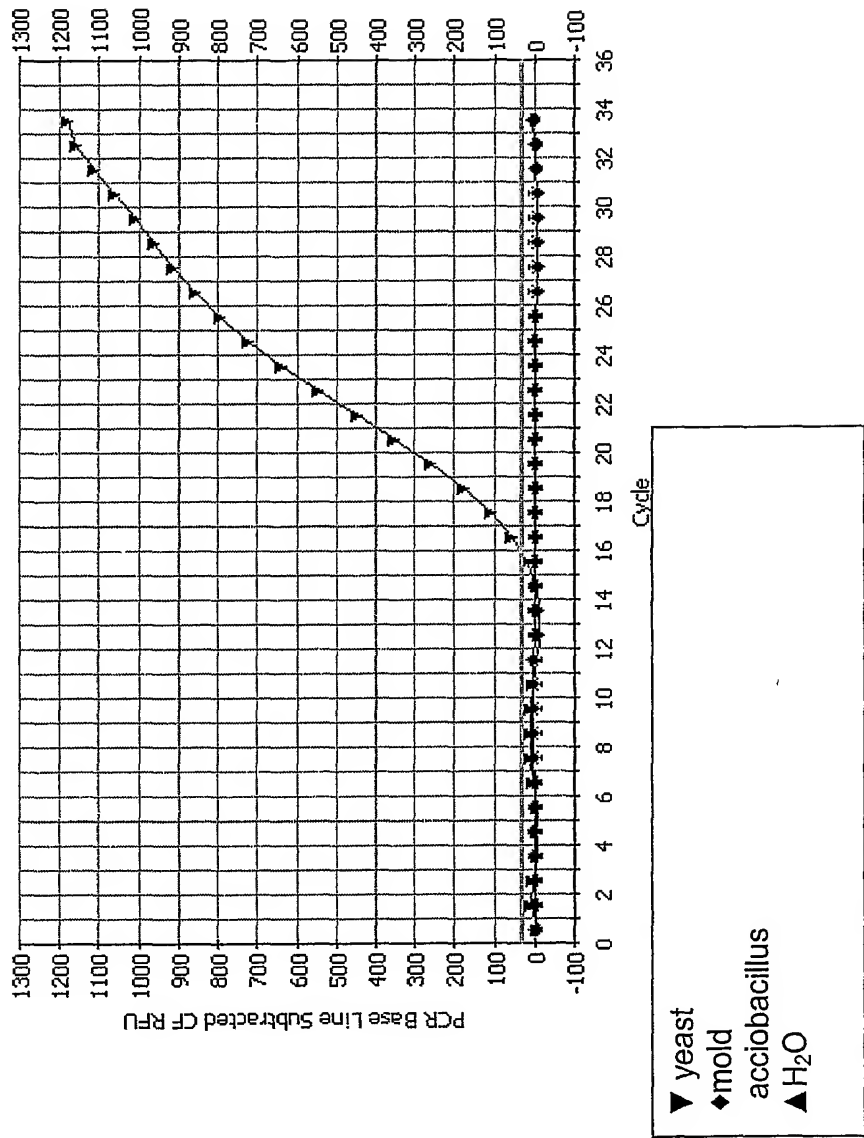


Figure 17

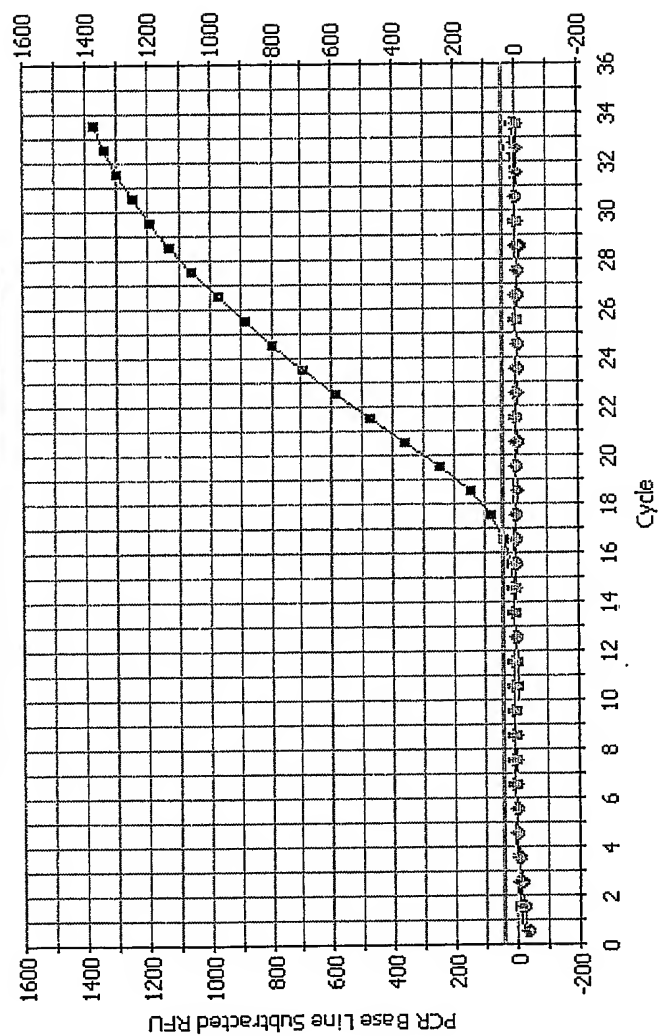
PCR Amp/Cycle Graph for FAM-490

Figure 18

PCR Amp/Cycle Graph for FAM-490

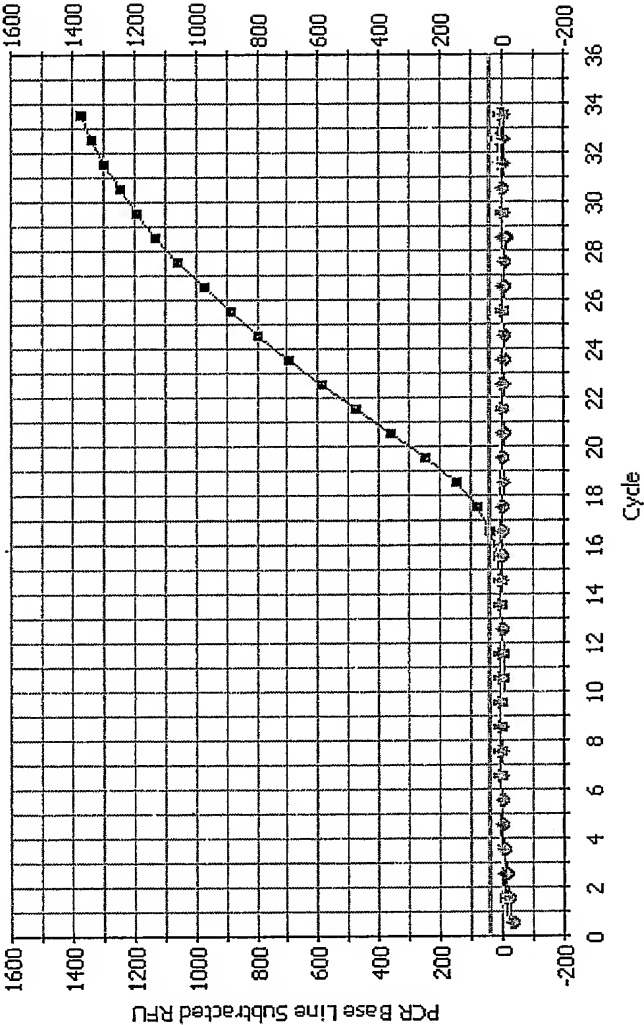


Figure 19
PCR Amp/Cycle Graph for FAM-490

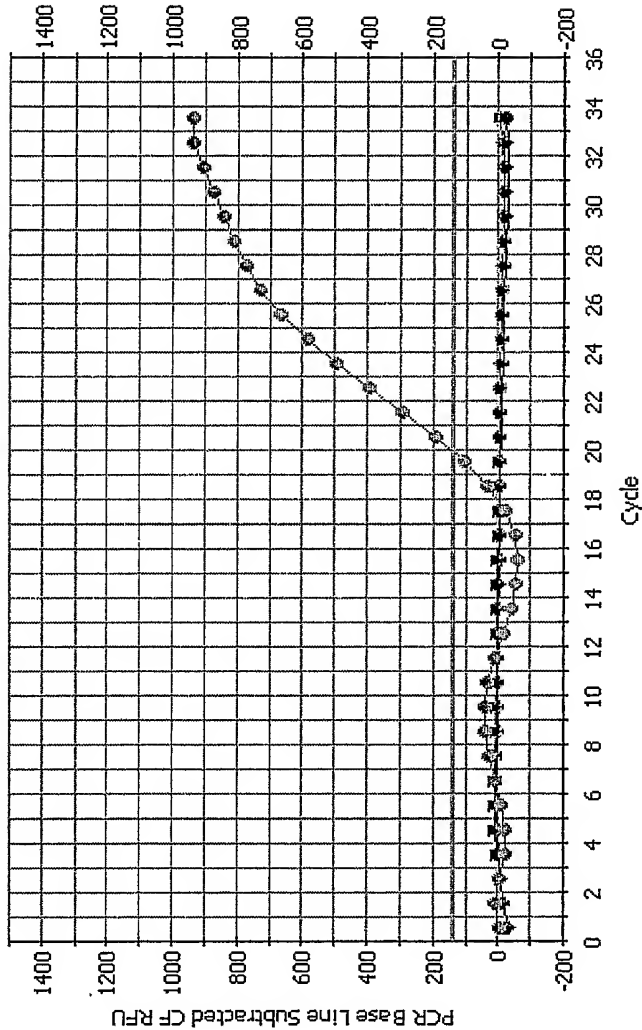


Figure 20

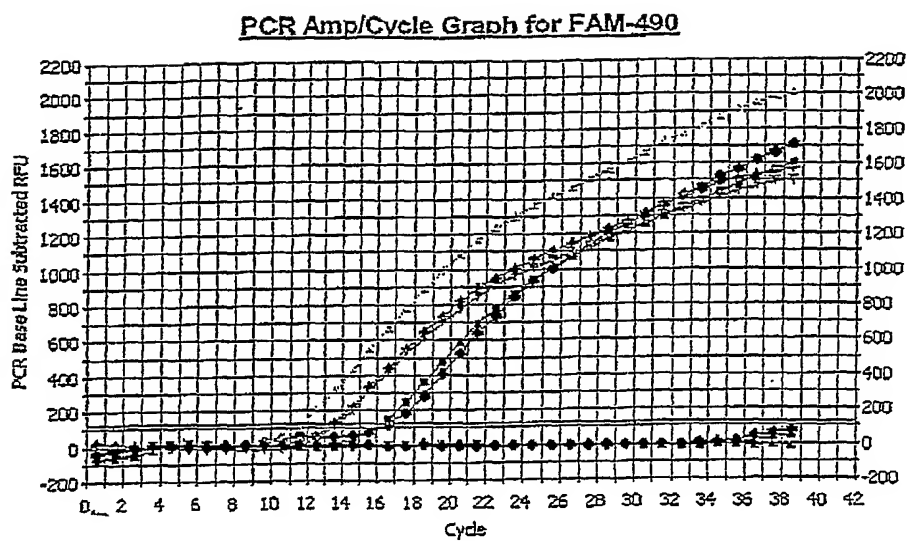


Figure 21

PCR Amp/Cycle Graph for FAM-490

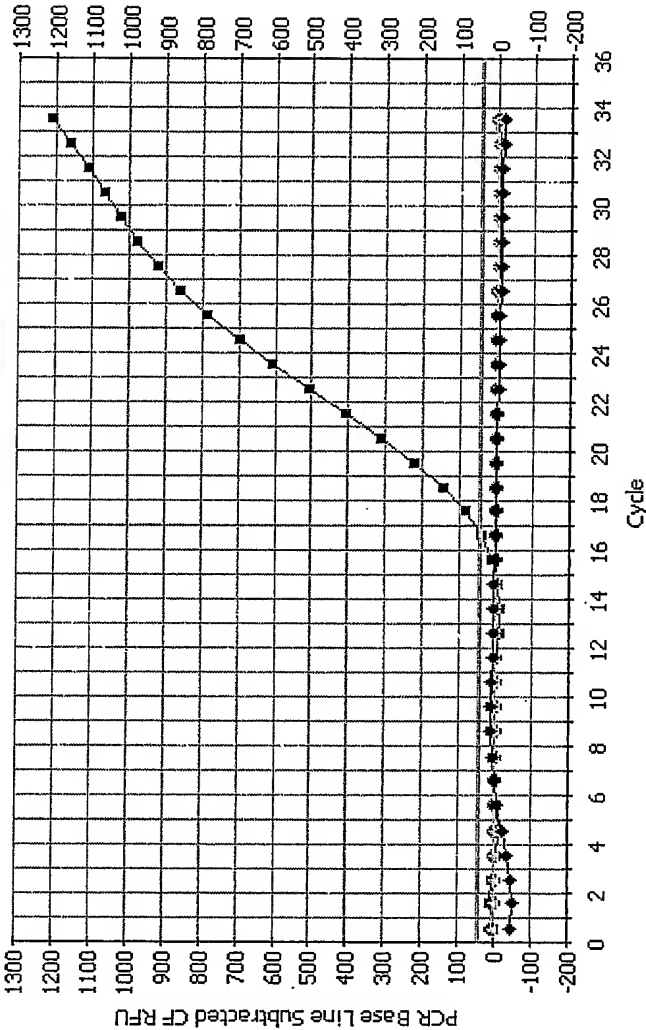


Figure 22

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1  CGTAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
2  CGTAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
3  CGTAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
4  CGTAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
5  CGTAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
6  CGTAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
7  CCCAGTTTCGGATTGAGGGCTGCAACTCGCCCCCATGAAGT
8  CTCAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
9  CGTAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC
10 CTCAGTTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGC

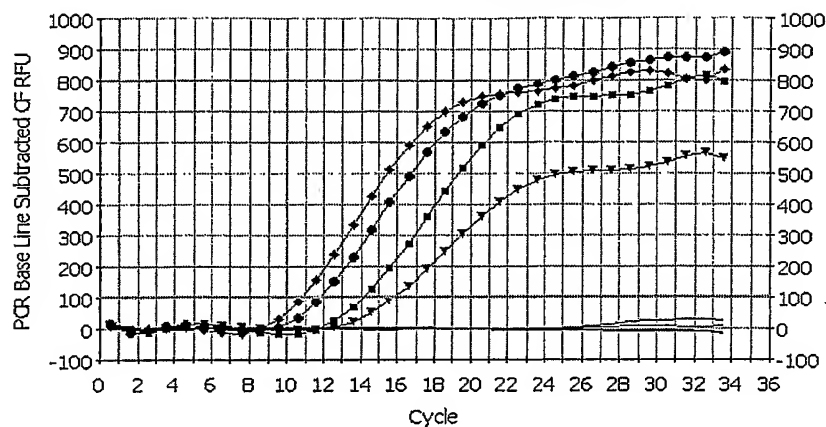
1  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTTC
2  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTTC
3  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTTC
4  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTTC
5  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTTC
6  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTTC
7  TGGAGTTGCTAGTAATCGCGGAATCAGCATGTCGCGGTGAATGCGTTTC
8  CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTTC
9  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTTC
10 CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTTC

1  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
2  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
3  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
4  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
5  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
6  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
7  CCGGGTCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
8  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
9  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
10 CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC

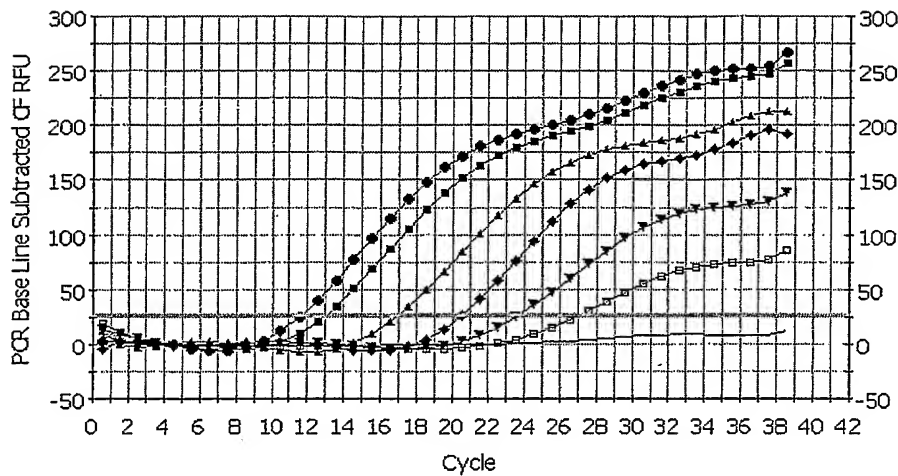
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^a 16S rDNA Sequences in the alignment are 16S rDNA sequences from the following organisms (GenBank accession numbers follow if applicable): 1) *A. acidocaldarius* strain ATCC 43030, 2) *A. acidocaldarius* strain DSM 454 (AB059664), 3) *A. cycloheptanicus* strain ATCC 49029, 4) *A. cycloheptanicus* strain DSM 4006 (AB042059), 5) *A. acidoterrestris* strain ATCC 49025, 6) *A. acidoterrestris* strain DSM 3923 (AB042058), 7) *Clostridium elmenteitii* isolate E2SE1-B (AJ271453), 8) *Geobacillus subterraneus* strain K (AF276307), 9) *Sulfobacillus disulfidooxidans* SD-11 (U34974), and 10) *B. thermoleovorans* strain ATCC 43513 (M77488) ^b

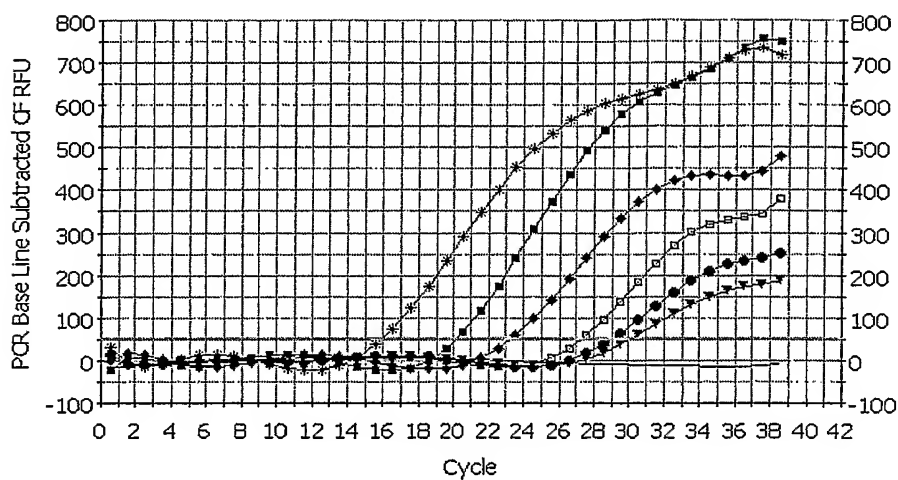
Note CC16S-R is in 5' to 3' orientation in alignment. Actual primer sequence is the reverse complement.

Figure 23

In addition, *G. stearotherophilus* ATCC 10149 (▼) can be detected. Curves below the base
 5 line include the blank control, *Lactococcus lactis* C2, *P. putida* 49L/51, and *E. coli* DH5 α . This
 is a representative curve of repeated trials.

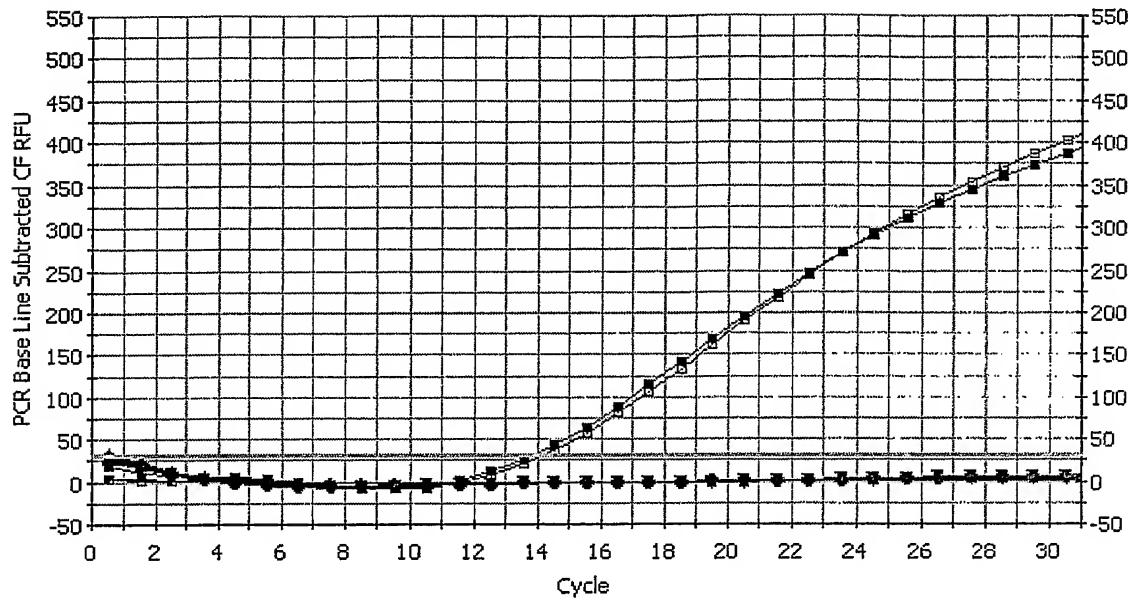
Figure 24

. Ten-fold serial dilutions were performed, and cell numbers^a represented at each curve are as follows: 1.6x10⁷ CFU/ml (●), 1.6x10⁶ CFU/ml (■), 1.6x10⁵ CFU/ml (▲), 1.6x10⁴ CFU/ml (◆), 1.6x10³ CFU/ml (▼), and 1.6x10² CFU/ml (□) appear above the baseline. The water control is below the baseline. This is a representative curve of repeated trials. ^a Cell numbers were calculated by finding the CFU/ml of plated samples and multiplying by the dilution level of the representative curve.

Figure 25

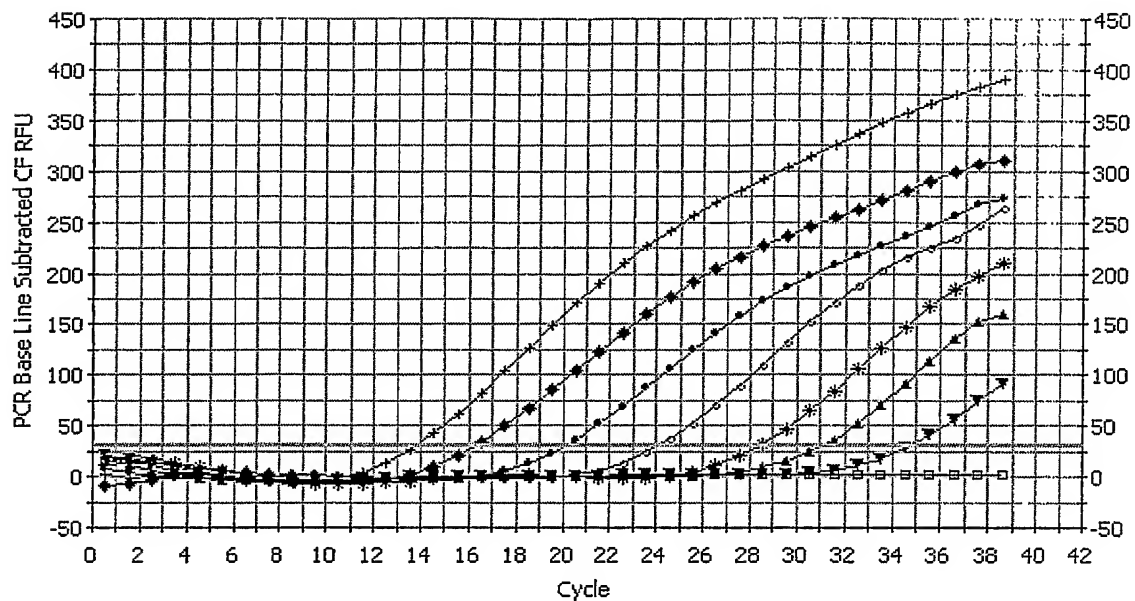
Cell counts at each curve are as follows: 6.3×10^6 CFU/ml (*), 6.3×10^5 CFU/ml (■), 6.3×10^4 CFU/ml (◆), 6.3×10^3 CFU/ml (□), 6.3×10^2 CFU/ml (●), and 6.3×10^1 CFU/ml (▼) appear above the baseline. The water control is below the baseline. This is a representative curve of repeated trials.

Figure 26



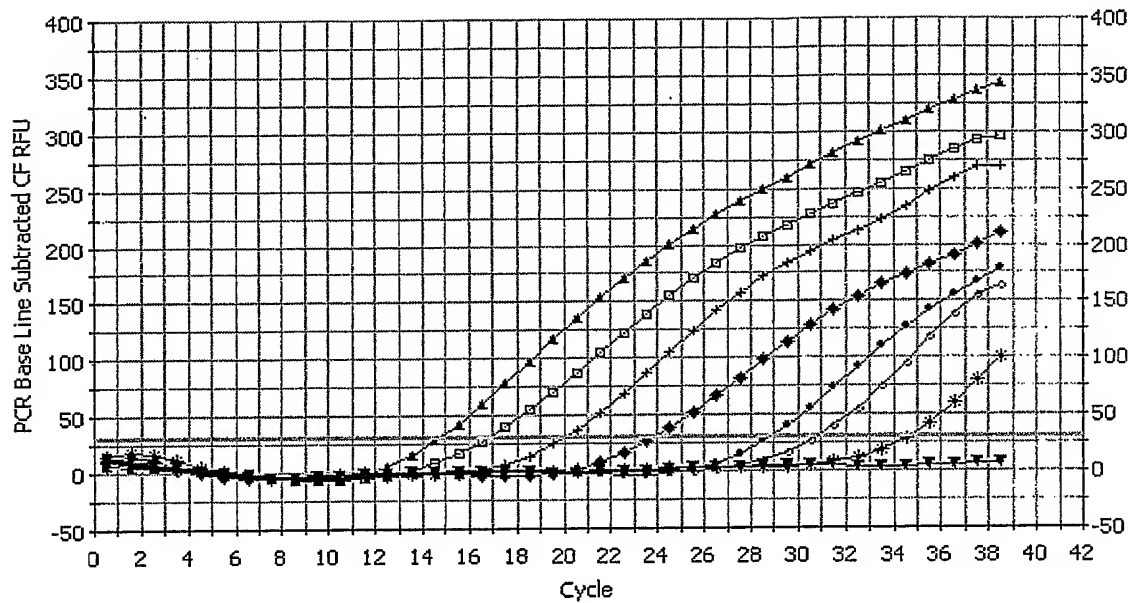
- 5 . *A. acidoterrestris* ATCC 49025 (■) , *A. acidocaldarius* ATCC 43030 (□), 6 other bacteria under the detection baseline: *Bacillus subtilis* OSU 456, *Pseudomonas putida* 49L/51, *E. coli* DH5α , *Listeria monocytogenes* V7, *Lactococcus lactis* ML3 and *Geobacillus* ATCC 10149 ■ *Alicyclobacillus acidoterrestris* ATCC49025 ; □ *Alicyclobacillus acidocaldarius* ATCC43030; + *Bacillus subtilis* OSU456; ● *E. coli* DH5α; ▲ *Pseudomonas putida* 49L/51; ▼ *Geobacillus* ATCC 10149; ♦ *Lactococcus lactis* ML3 ; ○ *Listeria monocytogenes* V7

Figure 27



- 5 ▲ 1ml saline with 4×10^6 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml saline with 4×10^5 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- + 1ml saline with 4×10^4 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ◆ 1ml saline with 4×10^3 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml saline with 4×10^2 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 10 ○ 1ml saline with 4×10^1 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- * 1ml saline with 4CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ▼ 1ml saline

Figure 28



5

◆: 10⁶ cells; □: 10⁴ cells; ▼: 10² cells; ●: bacterial medium (blank) control.
 ▲ 1ml apple juice with 4 × 10⁶ CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

□ 1ml apple juice with 4 × 10⁵ CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

10 + 1ml apple juice with 4 × 10⁴ CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

◆ 1ml apple juice with 4 × 10³ CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

● 1ml apple juice with 4 × 10² CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

○ 1ml apple juice with 4 × 10¹ CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

* 1ml apple juice with 4 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

15 ▼ 1ml apple Juice